## STIC-Biotech/ChemLib

From: Sent:

Rao, Manjunath N.

Monday, September 16, 2002 9:27 AM

To: Subject:

STIC-Biotech/ChemLib

Subject:

Sequence search request for 09/995,587

From: Manjunath N. Rao

Art Unit 1652, Room 10A11 Mail Box in Room 10C 01

Phone: 306-5681

Date: 9-16-02

Please search the following as soon as possible for application with serial number 09/995,587

SEQ ID NO: 2 and 10 against all commercial nucleic acid databases including issued patents database and pending application database and provide a print of all results.

SEQ ID NO:1 and 11, against all commercial protein databases including issued patents database and pending application database and provide a print of all results.

If y u have any questions please call me at the above phone number.

**Thanks** 

Manjunath N. Rao, Ph.D. Biotechnology Patent Examiner Art Unit 1652, Room 10A11 Crystal Mall 1, USPTO. SEP 16 2002

No 100 % or 65-100% matches for both DNA Sproken No matches for 15. a a regment was found.

Point of Contact P. Sheppard Searcher: Phone: Location: Date Picked Up: Date Completed: Searcher Prep/Review: Clerical: Dnline time:	TYPE OF SEARCH:  NA Sequences:  AA Sequences:  Structures:  Bibliographic:  Litigation:  Full text:  Patent Family:  Other:	VENDOR/COST (where applic.) STN: DIALOG: Questel/Orbit: DRLink: Lexis/Nexis: Sequence Sys.: WWW/Internet: Other (specify):
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staphylococ

09kil3 staphylococ 08648 staphylococ 09kil4 staphylococ 09ar7 staphylococ 09ar4 enterococcu 086919 staphylococ 095ar4 leuconostoc 091953 streptococcu 09fif5 enterococcu 070022 staphylococ

09fif5 enterococcu 070022 staphylococ 09kwx6 staphylococ 09a180 staphylococ 08648 staphylococ 091022 streptococc

09rpz2 streptococc 084941 streptococc 091bx1.acetobacter 093t54 streptococc 093t53 streptococc 068542 streptococc

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STRAIN=21042000: PubMed=11200435;
MEDLINP=21042000: PubMed=11200435;
Bezzate S., Aymerich S., Chambert R., Czarnes S., Berge O., Heulin T.;
Bezzate S., Aymerich S., Chambert R., Czarnes Gene impairs
"Disruption of the Peanibacilius polymyxa levansucrase gene impairs
"Its ablility to aggregate soil in the wheat rhizosphere.";
ENBL; AJ13373; CAB39277.1;
ENBL; AJ13373; CAB39277.1;
Thterpro; PRO03469; Glyco_hydro_68.
Fram: PF02435; Glyco_hydro_68.1.
SEQUENCE 499 AA; 55317 MW; E646CD986292336C CRC64;
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Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Paenibacillus.
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Result

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STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325; PubMed=11466286;

Glbson R., Ereton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

Glbson R.L., Sabathe F., Doucette-Stamm L., Wolf Y.I.,

Bennett G.N., Koonin E.V., Smith D.R.;

Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";

Sateriol. 183:4823-4838(2001).

EMBL; AE007686; AAK79737.1;
                                                                                                                                           188 LTDDQIKALNKMNFSKAAKSGTQMTYNDFQKIADTLIKQDGRYTVPFFKASEIKNMPAAT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 TKDAQTNTIEPLDVWDSWPVQDVRTGQVANWNGYQLVIAMMGIP-NQNDNHIYLLXNKYG 306
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Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 489;
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17.1%; Score 707; DB 16; Length 48
Best Local Similarity 37.2%; Pred. No. 9.5e-25;
Matches 183; Conservative 88; Mismatches 173; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          489 AA; 54553 MW; 9002CB364F1D3CD8 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                      489 AA.
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                                                                                                                                                                                                                                                                                                    PRT;
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Pfam; PF03435; Glyco_hydro_68.
Complete proteome.
SEQUENCE 489 AA.
                                                                                                                                                                                                                                                                                                             01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-DEC-2001 (TrEMBLrel, 19,
                                                                                                                                                                                                                                                                                              PRELIMINARY;
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21;
                             410 NIAMRDAHVIEDGNGDRYLVFEASTGL-ENYQGEDQIYNWLNYGGDDAFNIKSLFRILSN 468
                                         469 DDIKSRATWANAAIGILKLNKDEKNPKVAELYSPLISAPMVSDEIERPNVVKLGNKYYLF 528
                                                                                   529 AATRLNRGSNDDAMMNANYAVGDNVAMVGYVADSLTGSYKPLNDSGVVLTASVPANWRTA 588
                                                                                                                          372 TD---SRGSK----MINGISSKDIYMLGFSSKSLTGPYKPLNKTGLVLNLNLDPTDLTF 424
                                                                                                                                                                 Kurimoto M.;
"Cloning and sequencing of beta-fructofuranosidase gene from Bacillus sp. V30.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB010272; BAA32083.1;
Interpro; IPR003469; Glyco_hydro_68.
Pfam; PF02435; Glyco_hydro_68; 1.
SEQUENCE 487 AA; 53412 MW; 7F52A47921824AE3 CRC64;
                                                                                                                                                    589 TYSYYAVP-VAGKDDQVLVTSYMTNRNGVAGKGM----DSTWAPSFLLQINPDNTTTVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 MNFSKAAKSGT------QMTXNDFQK-----IADTLIKQDG-- 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 ---RYTVPFFKASEIKNMPAATTKDAQTNTIEPLDVMDSWPVQDVRTGQVANNNGYQLVI 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 AMMGIP-NONDNHIYLLYNKYGDNELSHWKNVGPIFGYNSTAV------SQEWSGSA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            336 VLNSDNSIQLFYTRVDTSDN-----NTNHQKIASATLYLTD-NNGNVSLAQVRNDYIVF 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MNFKRLAKKAAAVTFRTAILVGADGPHIFAQQMNSGDYKEDYGFAHITRAD-MLKIPGQQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.9%; Score 613.5; DB 2; Length 4: 34.0%; Pred. No. 1.6e-20; Live 81; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Tsusaki K.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                     Ol-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
BETA-FRUCTOFURANOSIDASE.
Bacillus sp.
Bacteria; Firmicutes; Bacillus/Clostridium group;
W.SIL-TaxID-1409;
                                                                                                                                                                                                                                                                                487 AA.
                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                       PRELIMINARY;
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Matches 168; Conservative
                                                                                                                                                                                              644 KMINQGDWIWDD 655
                                                                                                                                                                                                                477 SILOOGOLTIDN 488
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Created)
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(TrEMBLrel. 16, I
(TrEMBLrel. 19, I
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STRAIN-ATCC 12104, WVU45;
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                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                             Actinomyces naeslundii.
                                                                                                                                                                                                                                                                                      FRUCTOSYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 158; Conserva
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1655;
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                                                                                                                                                                                                                                                                                                                                                                                                                      naeslundii.
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             236 DGGDGTVYQNIQQFIDEGKWISGDNHTLRDPHYVED-KGHKYLVFEANTGTTDGYQGDQS 294
                                                           295 FNNKAYYGGSDVFFQNEKNKLLGSPK-KQIASLANGALGIVELADDY---TVKSVMKPLV 350
389 E-GDCYYYQTYDQWKATNK--GADNIAMRDAHVIEDGNGDRYLVFEASTG-LENYQGEDQ 444
                                                                                                          351 ASNIVADEVERANIFKMNNKWYLFIDSRGSKMTSD-----GINDKDVYMLGPGGDSL 402
                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325; PubMed-11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Glbson R., Lee H.M., Dubois J., Olu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Genome sequence and comparative analysis of the solvent-producing
J. Bacterium Clostridium acetobutylicum.";
Bacterium Clostridium acetobutylicum.";
EMBL; AE007686; AAK79739.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 TQMTYNDFQKIADTLIKQDGRYTVPF-----FKASEIKNMPAATTKDAQFNTI 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 EP-----LDVWDSWPVQDVRTGQVANWNGYQLVLAMMGIPN--ONDNHIYLLYNKYG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 DNELSHWKNVGPIFGYNSTAVSQEWSGSAVLNSDNSIQLFYTRVDTSDN--NTNHQKIAS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TKFSINVDKGGVHITNCSKHQVILEPDGVXYQTMQQ----AKGPIIXSFRDPXFFEDPKT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 TRKTY----KMISSLMVILAILTIPPLILRHNTGYTSIWSRQQAQNFKC--TKENTAPNI 56
                                             445 IYNWLNYGGDDAFNIKSLFRILSNDDIKSRATWANAAIGILKLNKDEKNPKVAELYSPLI
                                                                                            SAPMYSDEİERPNYVKLGNKYYLFAATRLNRGSNDDAWMNANYAVGD-NVAMYGYVADSL
                                                                                                                                       564 TGSYRPLNDSGVVLTASVPANWRTATYSYYAVPVAGKDDQVLVTSYMTNRN------
                                                                                                                                                                                                                                                                                                                                                     Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 ATLYLJDNNGNVŞLAQVRNDYIVFEGDCYYYQTYDQWKATNKGADNIAMRDAHVIEDGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.6%; Score 356.5; DB 16; Length 428; 27.2%; Pred. No. 5.4e-09; ative 70; Mismatches 176; Indels 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  428 AA; 48395 MW; 9670B154B178E23E CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                             428 AA.
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Pfam; PF02435; Glyco_hydro_68; 1.
                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                097179;
01-0CT-2001 (TrEMBLrel. 18,
01-0CT-2001 (TrEMBLrel. 18,
01-DEC-2001 (TrEMBLrel. 19,
LEVANSUCRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 27.29
Matches 125, Conservative
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SEQUENCE 428 AA:
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32;
DR-YLVFEASTG--LENYQGE---DQIY--NWLNYGGDDAFNIKSLFRILSNDDIKSRAT 476
                                                                                                                    325 -----KFTYAQGLNGVDGLYGFCGNSLRSNYKPLNGNGLVIIN--PINDPYQTYSWYL 375
                                                                                                          536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 IAVKSVTLGSGQVSAASDT---TIRTSANANSASSAANTQNSNSQVASSAAITSSTSSAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 SLNNTDSKAAQENTNTAKNDDTQKAAPANESSEAKNEPAVNVNDSSAAKNDD-QQSSKKN 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 QAGQAD---------QQAAGGAAAQDANGFKADNPGWANATKHTGAAHGVEEN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 -----PEQLTMP-----EISNGFPATSEDVW-------VWDYWTLTDEAAHQI-SYNGW 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 TLIKQDGRYTVPFFKASEIKNMPAATTKDAQTNTIEPLDVWDSWPVQDVRTGQVANWNGY 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLVIAMMGIPNQ----HDNHIY----LLYNKYGDNELS------HWKNVGPIFGYNS 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363 ---ASATLYLTDNNGNVSLAQVRNDYIVFEGDGYYYQTYDQWKATNKGADNIAMRDAHVI 419
                                                                                       477 WANAAIGILKLNKDEKNPKVAELYSPLISAPMVSDEIERPNVVKLGNKYYLFAATRLNRG
                                                                                                                                                                              537 SNDDAWMNANYAVGDN--VAMVGYVADSLTGSYKPLNDSGVVLTASVPANWRTATYSYYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bergeron L.J., Morou-Bermudez E., Burne R.A.;
"Characterization of the fructosyltransferase gene of Actinomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 TTAKLNK-DA---ENVVKKAGIDPNSLTDDQIKALNKMNFSKAAKSGTQMTYNDFQKIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     325 TAVSQ-----EWSGSAVLNSDNSIQLFYTRVDTS-----DNNTNHQKI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Actinomycineae; Actinomycetaceae; Actinomyces.
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22.7%; Pred. No. 4.6e-07;
ive 93; Mismatches 236; Indels 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF228582; AAG09737.1; -.
InterPro; IPR003469; Glyco_hydro_68.
Frans FP02435; Glyco_hydro_68; 1.
Transferase.
SEQUENCE 630 AA; 68256 MW: CPCAMAIRANDERD
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Last annotation update)
                             595 VPVAGKDDQVLVTSYMTNRNGVAGKGMDSTWAPSFLLQIN 634
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376 --VSGHDVLSFINEY--HFNGQLRYG--GTFAPT--LQIS 407
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364 RDQNNPSDPTEXMVFEGNSAFVREQQYVDAAAKAGQNTTLATCTEEDLGYEKGDPK 419 455DAFNIKSLFRILSNDDIKSRATWANAAIGILKLNKDEKNPKVAELYSPLISAPM 508	309
VSDEIERPNVVKLGNKYYLFAATRLNRGSNDDAWNNANYAVGDNVAMVGYVADSLTGS  : :   :     :      :      :      :      :	DD 354 QPEQTYSHCVMP QY 641 V 641 DD 407 V 407
	SULT 7
611 TNRNGVAGKGMDSTWAPSFLLQINPDNTTTVLAKMTN 647 	Q9AEX9; Q9AEX9; 01-JUN-2001 (TrEMBLrel 01-JUN-2001 (TrEMBLrel
RELIMINARY; Tremblrel	DT 01-0CT-2001 (TIEMBLEEL) DE LEVANSUCRASE. OS Rahnella aquatilis. OC Bacteria; Proteobacteri OC Rahnella.
. 19, . 19,	
Pseudomonas aurantiaca. Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; Pseudomonas. [1] TaxIb-86192; . SEQUENCE FROM N.A.	RT "Cloning and characteri. RL Submitted (FEB-2001) to DR EMBL, AYO27657; AAK1479, DR InterPro; IPR003469; G1, DR Pfam; PF02435; G1yco_hy, SQ SEQUENCE 415 AA; 4599
Koh I., Jang E.K., Kim J.S., Song K.S., Kim C.H., Rhee S.K.; "Screening, molecular cloning and characterization of a novel levansucrase, and its expression in Escherichia coli."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF306513; AAL09386.1; SEQUENCE 424 AA; 47009 MW; 9C1B4936A985162E CRC64;	Ouery Match Best Local Similarity 26 Matches 102; Conservative Qy 261 VWDSWPVQDVRTGQVANN Db 44 IWDAMPLRSL-DGTVVSVI
Č	Qy 310 LSHWKNVGPIE : :   :   :   :   :   :   :   :   :   :
TLIKQDGRYTVPFFKASEIKNMPAATT	Qy 361 KIASATLYLTDNNGNVSLA     : :   :    Db 156 TIAKVRGKVLTSEEGVTLA
HNGN	QY 417 HVIEDGNGDRYLVFEASTG   :     :     :   Db 206 PFIDPHDGKLYMVFEGNVA
	Qy 477 WANAAIGILKLNKDEK
G :	QY 534 NRGSNDDAWMANYAVG 
NIAAMRDAHVIEDGN-GDRYLVFEASTGLENYQGEDQIYNWLNYGGDDAFNIKSLFRILSN	Qy 590 YSYYAVPVAGKDDQVLVTS:             
9 DDIKSRATWANAAIGILKLNKDEKNPKVAELYSPLISAPMVSDEIERPNVVKLGNKYYLF 528	RESULT 8

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19;
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-AVARDEDGDD-WEMLPPLITANGVNDQTERPHFVFQDGKYYLF 308
                                 ANYAVGDNV----AMVGYVADSLTGSYKPLNDSGVVLTASVPAN 584
                                              DDQVLVTSYM----TNRNGVAGKGMDSTWAPSFLLQINPDNTTT 640
                                                                                               WNGYQLVIAMMGIPNQNDNHIYL------LYNKYGDNE 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.6%; Score 271.5; DB 2; Length 415;
16.6%; Pred. No. 3.6e-05;
.ve 60; Mismatches 132; Indels 89; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FFGYNSTAVSQEWSGSAV-LNSDNSIQLFYTRVDTSDNNTNHQ 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLENYQGEDQIYNWLNYGGDDAFNIKSLFRILSNDDIKSRAT 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KNPKVAELYSPLISAPMVSDEIERPNVVKLGNKYYLFAATRL 533
                                                                                                                                                                                                                                                                                                        ia; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                   ization of levansucrase.",
o the EMBL/GenBank/DDBJ databases.
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nydro_68; 1.
1958 MW: F09F5AlBF8690C5E CRC64;

    17, Created)
    17, Last sequence update)
    18, Last annotation update)

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|SFIDN 368
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SPECIES—Staureus (strain N315), and S.aureus (strain Mu50);
MEDLINE—21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cul L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Mizukami H., Hosoyama A.,
Sekimizu K., Hirakwa H., Kuhara S., Gotto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Whole genome sequencing of meticillin-resistant Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 AASLNNTDS-KAAQ-----BNTNTAKNDD---------TOKAAPA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATQVTTEEAPKAVQAPQTAQPANVETVKEEEKPQVKETTQPQDNSGNQRQVDLTPKKVTQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 NESSE-----AKNEPAVNVN-DSSAAKNDDQQSSKKNT--TAKLNKDAENVVKK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |::|
| 147 NGGTETQVEVAQPRTASESKPRVTRSADVAEAKEASDVSEVKGTDVTSKVTVESGSIEAP 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 PEIKNGSVVMATGEILGNGNIRYTFTNEIEHKVEVTANLEINLFIDPKTVQS----NGEQK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 VIAMM------GIPNQ--NDNHIYLLYNKYGDNELSHWKNVGPIFGYNSTA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 ITSKLNGEETEKTIPVVYNPGVSNSYTNVNGSIETFNK-ESNKFTHIAYIKPMNGNGSNT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----YTRVDTSDNN--TNHQKIASATLYLT 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 GGNKVEPHA--GQRVVLKYKLKFADGLKRG---DYFDF----TLSNNVNTYGVSTARKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 AG--IDPNSLTDDQIKALNKMNFSKAAKSGTQMTYNDFQKIADTLIKQDGRYTVPFF-KA
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Best Local Similarity 18.2%; Pred. No. 0.0003;
Matches 199; Conservative 151; Mismatches 301; Indels 442;
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                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-DEC-2001 (TrEMBLrel. 17, Last sequence update)
FNB PROTEIN (TIEMBLrel. 19, Last annotation update)
FNB PROTEIN (FIRROMECTIN-BINDING PROTEIN HOMOLOG)
STADINJONGONING TREATMENT OF T
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EMBL; AP003137; BAB43594.1; --

EMBL; AP003365; BAB58665.1; --

InterPro; IPR001999; Gram_pos_anchor.

InterPro; IPR001999; P.rich_extensn.

Pfam; PF00746; Gram_pos_anchor; 1.

PRINTS; PR01217; PRICHEXTENSN.

PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                  Staphylococcus aureus (strain N315), and
Staphylococcus aureus (strain Mu50).
Staphylococcus aureus (strain Mu50).
Bacillus/Staphylococcus group; Staphylococcus
NCBI_TaxID=158879, 158878;
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                       1038
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                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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SEQUENCE 1038 A
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                                                                                                                                                                                                                                                                                                                                                                                                             Hettwer U., Jaeckel F.R., Boch J., Meyer M., Rudolph K., Ullrich M.S., "Cloning, nucleotide sequence, and expression in Escherichia coli of levansucrase genes from the plant pathogens Pseudomonas syringae pv. glycinea and P. syringae pv. phaseolicola."; Appl. Environ. Microbiol. 64:3180-3187(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----VGPIFGYNSTAVSQEWSGSAV-LNSDNSIQLFYTRVDTSDNNTNHQKIASATLYL 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             characterization and Mutational Analysis of Three Allelic 1sc Genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFEASTGLENYQGEDQIYNWLNYGGDDAFNIKSLFRILSNDDIKSRATWANAAIGILKLN 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 VFEG-----NVAGE-----RGSHTVGAAELGPVPPGHEDVGGARFQVGCIG-LAVA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            489 KDEKNPKVAELYSPLISAPMVSDEIERPNVVKLGNKYYLFAATRLNRGSNDDAMMNANYA 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 VRTGQVANWNGYQLVIAMMGIPNQNDNHIYLLYN------KYGDNELSHWKN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             549 VGDNV----AMVGYVADSLTGSYKPLNDSGVVLTASVPANWRTATYSYYAVPVAGKDDQV
                                                                                                                                                                                   Pseudomonas syringae (pv. glycinea).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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23.6%; Pred. No. 0.0001;
Live 72; Mismatches 166; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Encoding Levansucrase in Pseudomonas syringae.";
J. Bacteriol. 183:3282-3392(2001).
EMBL: AF346402; AAK49952.1;
Transferase; Glycosyltransferase.
SEQUENCE 431 Aa; 47619 MW; 0C71D0F133071AA5 CRC64;
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                                                                                   Last sequence up
                                                        Created)
        PRT;
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                                               01-DEC-2001 (TrEMBLRel. 19, Creat 01-DEC-2001 (TrEMBLRel. 19, Last 01-DEC-2001 (TrEMBLRel. 19, Last LEVANSUCRASE LSCC (EC 2.4.1.10).
PRELIMINARY;
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Best Local Similarity 23.6°
Matches 108; Conservative
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                                                                                                                                                                                                                                                                            NCBI_TaxID=318;
                                                                                                                                                                                                                                                                                                                                                          STRAIN-PG4180;
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52;

DNGSYSLNLDKLDKTYVI-----HYTGEYLQ-----GSDQVNFR-----------------466

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셤 å RESULT Q99RD2

us-09-995-587a-1.rspt

940 AA; 103555 MW; E35FBBCA907AE345 CRC64;

SEQUENCE

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KSRATWANAAIGILKLNK 489                     -YRLTWDNGLVLYSNK 500		TEENQDNTPLDI 550	_				: :  :: [GVIEEIEENS 728	672	QIHGQNKGDQSF 787		MQFGGHNSVDFE 847		PETP-TPPTPEV 906	751 KPVPPAKEEPKK 965		  FGGLFS			ins in
430 FEASTGLENYQGEDQIYNWLNYGGDDAFNIKSLFRILSNDDIKSRATWANAALGILKLNK 	490 DEKNPKVAELYSPLISAPMVSDEIERPNVVKLGNKYYLFAATRLNRGS-			558LTAS	DEESTKG	594 AVPVAGKDDQVLVTSYMTNRNGVAGKGMDSTWAPSFLLOINPDN	671 TTESNLIELVDELPEEHGQAQGPIEEITENNHHISHSGLGTENGHGNY		HVDIKSELGYEGGONSGNQSFEEDTE	0/3GERDKPVDWDLIG-YGLKPHD		EDTI.PKVSGONEGOOTTEEPINGEBURGERINGERINGERINGERINGERINGERINGERINGERI		/23 PGTPQTPNTPNTPEIPLTPETPKQPETQT	752NNRLPQTGNNANKAMIGLGMGTLLS	966 PSKPVEQCKVVTPVIEINEKVKAVAPTKKAQSKKSELPETGGEESTNKGML	777 MFGLAEINKRRFN 789		602.682 PRELIMINARY; PRT; 940 AA. 053682 OCTEMBLED. 01, Created) 01.NOV-1996 (TrEMBLED. 01, Last sequence update) 01.DEC-2001 (TrEMBLED. 19, Last annotation update) FIBRONECTIN BINDING PROTEIN B. Staphylococcus aureus. Bacillus/Staphylococcus group; Staphylococcus. NCBL_TAXID-1280; CABLINS/Staphylococcus group; Staphylococcus. NCBL_TAXID-1280; CABLINS/Staphylococcus group; Staphylococcus. NCBL_TAXID-1280; CABLINS/Staphylococcus group; Staphylococcus. NCBL_TAXID-1280; CABLINS/Staphylococcus group; Staphylococcus. NCBL_TAXID-1280; CABLINSON N.A. STRAIN-8325-4; MEDLINE-20111475; Pubmed-1837266; JORSSON K., Signas C., Muller H.P., Lindberg M.; Two different genes encode fibronectin binding proteins Staphylococcus aureus. The complete nucleotide sequence characterization of the second gene."; ENEL: X62992; CAA44726-1; InterPro; IPRO01899; Gram_Pos_anchor. Pfam: PPO0286; Fr. bind; 2. Pfam: PPO0286; Gram_Pos_anchor; 1. PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN 1.
Oy GD	ço q	ð	g	δ	g	ογ	පු	ð i	g :	S 8	3 8	S 8	å	<u>5</u> 8	ογ	QQ	δ	<b>a</b>	RESCULT  OS 3662  ID 063662  ID 063662  DT 011  DT 01  D

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44;
                                                     55 VTLGSGQ-----VSAASDTTIRTSANANSASSAANTQNSNSQVASSAAITSSTSSAASLN 109
                                                                                                         110 NTDSKAAQENTNTAKNDDTQKAAPANESSEAKNEPAVNVND--SSAAKNDDQQSS---- 162
                                                                                                                            138 KPRMKRSTDVTAVAEKEVVEETKATGTDVTNKVEVEEGSEIVGHKQDTNVVNPHNAERVT 197
                                                                                                                                                                                                                                   198 LKYKWKFGEGIKAG---DYFDF-TLSD-----NVETHGISTLRKVPEIKSTDGQV- 243
Query Match
6.0%; Score 246; DB 2; Length 940;
Best Local Similarity 18.6%; Pred. No. 0.0013;
Matches 185; Conservative 135; Mismatches 334; Indels 340; Gaps
                                                                                                                                                               ----KKNT--TAKLNKDAENVVKKAGIDPNSLTD---------------------------DQIK 194
                                                                                                                                                                                                                  195 ALNKMNFSKAAKSGTQMTYNDFQKIADTLIKQDGRYTVPFFKASEIKNMPAATTKDAQTN 254
                                                                                                                                                                                                                                                                      255 TIEPLDVWDSWPVQDVRTGQVANWN--------GYQLVIAMMGIPNQN 294
                                                                                                                                                                                                                                                                                                 295 DNHIYLLYNKYGDNELSHWKNVGPIFGYNSTAVSQEWSGSAVLNSDNSIQLFYTRVDT-- 352
                                                                                                                                                                                                                                                                                                                                                353 -SDNNTNHQKIASATLYLTDNNGNVSLAQVRNDYIVFEGDGYYYQTYDQWKATNKGADNI 411
                                                                                                                                                                                                                                                                                                                                                                                                          330 KVDGKFSH-----FAYMKPNNQSLSSVTVTGQVTKGNKPGVNNPTVKVYK--HIGSDDL 381
                                                                                                                                                                                                                                                                                                                                                                                                                                    412 A-----MRDAHVIEDGNGDRYLVFEASTGLE-NYQGEDQIYNWL----NYGGDDAFNIK 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 FQTHLFGYYNYYYTSNLTWRN---GVAFYSNNAQGDGKDKLKEPIIEHSTPIELEFKSEP 498
                                                                     517 NVVKLGNKYYLFAATRLNRGSNDDAWMNANY------AVG--------550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        499 PVEK-----HELTGTIEESNDSKPIDFEYHTAVEGAEGHAEGTIETEEDSIHVDFEES 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   551 -----DNVAMVGYVADSLIGSYKPLNDSGVV------LTASVPANWRIATYSYYA 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           639 TTVLAKM-----TNQGDWIWDDSSENLDM------IGDLDSAALP------ 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              670 VDIKSELGYEGGQNSGNGSFEEDTEE-DKPKYEQGGNIVDIDFDSVPQIHGQNNGNQSFE 728
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386 PELKQLEEERAHSKLKQVVEDFRKKFKTSEQVTPKKRVKRDLAANENNQOKIELTVSPENI 445
                                                                                                                                                                                                                                                                                                       291 PNQNDNHIYLLYNKYGDNELSHWKNYGPIFGYNSTAVSQEWSGSAVLNSDNSIQLFYTRV 350
                                                                                                                                                                                                                                                                                                                                     446 TVYEGEDVKFTVTAKSDSKTT--LDFSDLLTKYNPSVSDRISTNYKTNTDN-----HKIA 498
                                                                                                                                                                                                                                                                                                                                                                                               351 DTSDNNTNHQKIASATLYLTDNNGNVSLAQVRNDYIVFEGDGYYYQTYDQWKATNKGADN 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         706 YFLTPFNKIKQIVDDLDKKVEQDQPA------PIPENSEMDQAKEKAKIAVSKYMS 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        672 PGERDKPVDWDLIG-----YGLK---PHDPATPNDPETPTTPETPETPNTPKTPK 718
                          179 KK-----AGID---PNSLTDDQIKALNKMNFSKAAKSGTQMTYNDF----QKIAD--
                                                                   270 KKETSSEENTQKVDEHYANSLQNLAQKSLEELDKATTNEQATQVK-NQFLENAQKLKEIQ
                                                                                                                    222 TLIKQDGRYTVPFFKA-----SEIKNMPAATTKDAQTNTIEPLDVWDS-----
                                                                                                                                                                                                                       ---WPVQDVRTGQVANWNGYQ----LVIAMMGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leuconostoc mesenteroides.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                              :: | :: | :: 4 | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            508 MVSDEIERP-----NVVKLGNKYYLFAATRLNRGSNDDAMMNANYAVGDNVAMVGYVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                646 FMNYQLHAQMEMLTRKVVQYMNKYPDNAEIKKIFESDMKRTKEDNYGSLENDALKGYFEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   562 SLTGSYKPL----NDSGVVLTASVPANWRTATYSYYAVPVAGKDDQ-----VLVTSYMT
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MEDLINE-20169623; PubMed-10705445;
Funane K., Mizuno K., Takahara H., Kobayashi M.;
Fune encoding a dextransucrase-like protein in Leuconostoc mesenteroides NRR B-512F.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    545 PEQKDSKTEEKVPQEPKSNDKNQLQELIKSAQQELEKLE------
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DEXTRANSUCRASE.
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EMBL; AB020020; BAA90527.1; -
HSSP; P06278; 1VJS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specificity for serum 1947;
Eur. J. Immunol. 20:2241-2247(1990).
Eur. J. Immunol. 20:2241-2247(1990).
CAPABILITY AND A REGION CORRESPONDING TO THE BETA ANTIGEN.
EMBL. X58400; CAA41384.1;
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR001899; Ig.
SWART; SW00746; Gram_pos_anchor.
SWART; SW00746; Gram_pos_anchor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heden L., Frithz E., Lindahl G.;
"Molecular characterization of an IgA receptor from group B streptococci: sequence of the gene, identification of a proline-rich with unique structure and isolation of N-terminal fragments but J Immunol. 21:1481-1490(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMUNOGLOBULIN ALPHA FC RECEPTOR.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 NNT-----KAAPANESSEAK- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 NETNRLLHIKQHEEVEKDKKAKQQ--KTLKQSDTKVDLSNIDKELNHQKSQVEKMAEQKG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 --NEPAVNVNDSSAAKNDD-----QQSSKK-----------NTTAKLNKDAENVV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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30 TRIPEPTIDE REPEATS (MOTIF XPZ).
W; FC10A200B3DB7CE1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lindahl G., Akerstroem B., Vaermann J.-P., Stenberg L.; Characterization of an IgA receptor from group B streptococci:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWART: SW00409; IG; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
Receptor; Signal; Transmembrane; Repeat; Cell wall; Virulence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 5.8%; Score 237.5; DB 2; Length 1
Best Local Similarity 20.1%; Pred. No. 0.0038;
Matches 189; Conservative 129; Mismatches 349; Indels
                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
IMMUNOGLOBULIN ALPHA FC RECEPTOR PRECURSOR.
907 TGGEESTNNGML---FGGLFSILGLALLRRNKKN 937
                                                                                                                         PRT; 1134 AA
                                                                                                                                                                    01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91257158; PubMed-2044657;
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MEDLINE=91055597; PubMed=2242758;
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1134 AA; 127980
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                                                                                                                                                                                                                                                                                  Streptococcus agalactiae.
                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 39-56.
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-1311;
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1002
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                                                                                                             099051
                                                                   RESULT 11
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SPECIES-S. Gureus (strain N315), and S. aureus (strain Mu50);
MEDLINE-21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cul L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,
Mizutani Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 VTLGSGQ-----VSAASDTTIRTSANANSASSAANTQNSNSQVASSAAITSSTSSAASLN 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 EQPSKSTQVTTEEA---PTTVQAPKVETEMKSQEDLPSEKVADKETTGTQVDIAQPSNVS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 NTDSKAAQENTNTAKNDDTQKAAPANESSEAKNE--PAVNVND------SSAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 EIKPRMKRSADVTAVSEKEVAEEAKATGTDVTNKVEVTESSLEGHNKDSNIVNPHNAQRV 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 NERTIRYTFTDYINNKKDLTAELNLNIFIDPTTVTKQGSQKVEVTLGONKVSKEFDIKYL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 WPVQDVRTGQVANWNGYQLVIAMMGIPNQNDNHIYLLYNKYGDNELSHWKNVGPI-FGYN 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STAVSQEWSGSAVLNSDNSIQLFYTRVDTSDNNTNHQKIASATLYLTDNNG-NVSLAQVR 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      544 AEGIIETEEDSIHVDFEESTHENSKHHADVVEYEEDTNPGGGQVTTESNLVEFDEESTKG 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 IVVGMGQEKEAAASEQNNTTVEESGSSATESKASETQTTTNNVNT---IDETQSYSATST
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                                                                                                                                                                                                                                                                                                                                                                                             961 AA; 106010 MW; 364940F884EA4101 CRC64;
                                                                                                                                                                                                                                                     Lancet 357:1225-1240(2001).

EMBL; AP003137; BAB43593.1;

EMBL; AP003137; BAB43593.1;

InterPro; IPR001899; Gram_pos_anchor.

InterPro; IPR002965; P_rich_extensn.

PRINTS; PR001217; PRICHEXTENSN.

PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.

SEQUENCE 951043; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.6%; Score 231.5; DB 16; Best Local Similarity 19.9%; Pred. No. 0.0059; Matches 199; Conservative 121; Mismatches 349;
                     Bacillus/Staphylococcus group: Staphylococcus.
NCBI_TaxID=158879, 158878;
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                                                                                                           37;
                                                                                                                                                                                                       52 VKSVTLGSGQVSAASD-----TTIRTSANANSASSAANTQNSNSQVASSAAITSSTSSA 105
                                                                                                                                                                                                                                                                             111 TAATSTEDKAATTADTSTEDKATTTAATSTEDKATTTAATSTEDKAATTTOATSTEDKAAT 170
                                                                                                                                                                                                                                                                                                           154 ---AKNDDQ-----QSSKKNTTAKLNKDAENVVKKA-GIDPNSLTDDQIKALNKHNFSK 203
                                                                                                                                                                                                                                                                                                                                                                       204 AAKSGTQMTYNDFQKIADTLIKQDGRYTVPFFKASEIKNMPAATTKDAQTNTIEPLDVWD 263
                                                                                                                                            231 KTIDGKTYYYDD-----DDQVK-------KNF--ATVIDGKVLYF----- 261
                                                                                                                                                                                                                                                                                                                                                                                                                                     264 SWPVQDVRTGQVANWNGYQLVIAMMGIPNQNDNHIYLLYNKYGDNELSHWKNVGPIFGYN 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 -----DKETGALADTNDYQFLEGL-----TSENNTYTEHNASVGTTSDSYTNVD----GY- 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 STAVS------OEWSGSAVLNSDNSIQLFYTRVDTSDNNTNHQKIASATLYLTDN 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 LTADSWYRPKDILVNGONWESSKDDDLRPLLMTWWPDKATQVNYLNAMKYLDATETET-- 365
                                                                                                                        429 ------VFEASTGLENYQGEDQIYNWLNYGGDDAFNIKSLFRILSNDDIKSRATW 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  527 LFAATRLNRGS--NDDAWMNANY-----AVGDNV--AMVGYVADSLTGSYKPLNDSGVV 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 547
                                                                                                                                                                                                                                                ASLINNTDSKAA-----QENTNTAKNDDTQKA---APANESSEAKNEPAVNVNDSSA-
                                                                                                                                                                                                                                                                                                                               373 NGNVSLAQVRNDYIVFEGDGYYYQTYDQWKATNKGADNIAMRDAHVIEDGNGDRYL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----VYTSDDSQDALNKAAQNIQVKIEEKISQEGQTQWLKDDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNQHVSILEDWSDNDAEY----VKDNGDNQLSMDNKLRLSLKYSLTMPAVDQYGNKRSGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              577 LT--ASVPANWRTATYSYYAVPVAGKDDQVL-------VTSYMTNRNGV
                                                                                                         233;
                                                                       Length 1016;
                                                          Ouery Match 5.7%; Score 236.5; DB 2; Length 1 Best Local Similarity 21.2%; Pred. No. 0.0037; Matches 162; Conservative 103; Mismatches 266; Indels
Pfam; PF02324; Glyco_hydro_70; 1.
SEQUENCE 1016 AA; 110344 MW; 8896EFDE13CCCB47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----AGKGMDSTWAPSF-LLQINPDNTTTVLAKMTNQ 648
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last sequence update)
FNBB PROTEIN (FIBRONECTIN BINDING PROTEIN HOMOLOG).
Staphylococcus aureus (strain N315), and
Staphylococcus aureus (strain Mu50).
Bacteria: Firmicutes; Bacillus/Clostridium group;
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Indels 331; Length 961;

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604 IVTCANSDHITTYPEDTKEYTIESNLIEL-VDELPEEHGOAGGFI		Qy 260 DVWDSWPVQDVRTGOVI	Db 1021 QFTEDIDIGYII	QY 320 FGYNSTAVSQEWSGSAV	Db 1065SSGAVSVRLSGGAG	Qy 380 QVR	RTTT	DD 1171 NEKSDIADVSAVCAVOT	471	Db 1211DEFVTIAEM	515 RPN 	Db 1263 RTETIELOKENHLIPGS	QY 565 GSYKPLNDSGVVLTASVI	DD 1317ENGQVVVTDLKE	QY 598AGKDD	Db 1371 PGSVQLVKVDADDAAITL	QY 614 NGVAGKGMDSTWAPSFLL	1431	Db 1490 LDEEGNVLREGIRTGENG		Db 1550 TLVFENKLTPEVPESPEN	Oy 741 PETPKOPETOTNNRLP	Db 1610 DKNPEKSSDSNNRIDRLPK	RESULT 15	50A7 091	Q9LQA7; 01-OCT-2000	D1 01-OCT-2000 (TrEMBLrel. D1 01-DEC-2001 (TrEMBLrel. DE FAN2 10						
O O O O O O O O O O O O O O O O O O O	604 IVTGAVSDHTTVEDTKEVEREN	517 NVVKLGKKYYLFAATRLNRGSNDDAWMNANYAVGDNVAMYGYVADSLTGSYK	652 NHHISHSGLGTENGHGNY-GVIDEIEENSHVDIKSELGYEGGQNSGNQSFEEDTEEDK	569 PLNDSGVVLTASVPANWRTATYSYYAVP-VAGKDDQVLVTSYMTNRNGVAGKGMDSTW-A	7.9 FAXEQGGNIVDIDFDSVPQIHGQNNGNQSFEEDTEEDK	747 PKYEQGGNIIDIDFSYPOHGG-FRENETREPARTED   1   1   1   1   1   1   1   1   1	673GERDKPVDWDLIGYGIRPHDD&MDWNDRMMANALLEDINKDKPNYQFGGHNSVDFEEDTLPKV	806 SGQNEGQOTIEEDTTPPTPPTPEVPSEPETP-TPPTPFPFPFPFPFPFPFPFPFPFFPFFFFFFFFFF	728 TPWTPWTPEIPLTPETPKOPETOT	863 TP-VPPTPEVPSEPGKPVPPAKEEPKKPSKPVEQGKVVTPVIEINEKVKAVAPTKQKOSK	752 NNRLPQTGNNANKAMIGLCMGTLLSMFGLAEINKRRFN 789		RESULT 14 09KEWO	Q9KFWO PRELIMINARY; PRT; 1661	01-OCT-2000 (TrEMBLrel. 15, Created)	01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17, BH0361 BBOTEL	BH0361.			JIMAIN-C-125 / JCM 9153; MEDLINE-2012582; PubMed-11058132;	Janami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.		halodurans and genomic sequence comparison with Bacillus Nucleic Acids Res. 28:4317,4331(2000).			SEQUENCE 1661 AA; 183657 MW;	5.6%; Score 230; DB 16.	20.4%; Pred. No. 0.013; '	VASSAAITSSTSSAASLNNTDSKAAQENTNTAKNDDTOKAAPANESSEAKNEPAVNVNDS 151	IDSAYWITFKTSLEDTLIKSNYPNRATLKSDNAEDFNVDAS	SAAKNDDQQSSKKNTTAKLNKDAENVVKRAGIDPNSLTDDQIKALNKMNFSKAAKSG   :- : 	NINFSQSSISNAKI	

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\GTGSGETGSLEVTKVDADTG----EVLQGATFTLYDSEGEFAIR 1117
                                                                                                                         LYGDYLLKEDSAPEGYLVGINDTQRVT---IDTV----LHEVTVE 1170
                                                                                                                                                                             : ||:
|METDEBGIVFAGSLEPGDYGFVELNAPVGYKLDETPVVFTVEED 1262
VANWNGYQLVIAMMGIPNQNDNHIYLLYNKYGDNELSHWKNVGPI 319
                                                     AVLNSDNSIQLFYTRVDTSDNNTNHQKIASATLYLTDNNGNVSLA 379
                                                                                                                                                                                                                                                                                      KPGEYQEVETKAPAGYELEATPIGFTIERNQQEVATVAVENHLI 1370
                                                                                                       -- NDYIVFEG---- DGYYYQTYDQWKATNKGADNIAMRDAH--VIE 420
                                                                                                                                                            ---FEASTGLENYQGEDQIYNWLNYGGDDAFNIKSLFRILSNDD 470
                                                                                                                                                                                                                                                                                                                                                                                           LNKDEK------NPKVAELYSP----LISAPMV-SDEIE 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATRLNRGSNDDAWMNANYAVG------DNVAMVGYVADSLT 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....VULVTS-----YMTNR 613
                                                                                                                                                                                                                                                                                                                                                                                                                              LQINPDNTTTV----LAKMTNQGDWIWDDSSE--N 659
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ae; Streptophyta; Embryophyta; Tracheophyta;
ophyta; eudicotyledons; core eudicots; Rosidae;
es; Brassicaceae; Arabidopsis.
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|PQTGEEFLTFLILGL--LLMTAGGVLLLKRR 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTGNNANKAMIGLGMGTLLSMFGLAEINKRR 787
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15, Last sequence update)
19, Last annotation update).
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EMBL; AC008262; AAF27056.1; -
InterPro; IPR002965; P_Tich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 138 AA; 13864 MW; B2EDEDA7E272A50A CRC64;
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0; Gaps Query Match 5.4%; Score 224; DB 10; Length 138; Best Local Similarity 60.9%; Pred. No. 0.0015; Matches 42; Conservative 0; Mismatches 27; Indels (

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P40442 048247 003174 048245 P45384 P75384 P75075 P29336 P45508 P16053 053654 P11137

gallus gall staphylococ

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RT Sequence analysis of the Streptococcus mutans fructosyltransferase RL Sequence analysis of the Streptococcus mutans fructosyltransferase RL J. Bacteriol. 170:810-816,1989.

"I Bacteriol. 170:810-816,1989.
"I SAMIAKITY: SUCROSE + (2,6-BETA-D-FRUCTOSYL)(N) = ALSO ACT AS FRUCTOSYL ACCEPTORS).

"I SUBCELLUIAR LOCATION: Secreted.
"I SIMILARITY: BELONGS TO FAMILY 68 OF GIXCOSYL HYDROLASES.
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                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus mutans.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MYKSGKNWAVVTLSTAALV-FGATTVNASADTNIENNDSSTVQVTTGDNDIAVKSVTLGS 59
                                                                                                                                                                                                                                                                                                 01-0cT-1989 (Rel. 12, Created)
01-0cT-1989 (Rel. 12, Last sequence update)
15-DEC-1988 (Rel. 37, Last annotation update)
Levansucrase precursor (EC 2.4.1.10) (Beta-D-fructofuranosyl transferase) (Sucrose 6-fructosyl transferase).
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6DDE057465DB4042 CRC64;
                                                                                                                                                                                                                                                                                     797 A.A.
                                                                                                                                                                                                                  ALIGNMENTS
               YIQQ_YEAST
VAC1_HELPY
FRUA_STRMU
VAC2_HELPY
IGA2_HAEIN
STFR_ECOLI
GTFS_STRDO
VAC3_HELPY
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PIR; B28551; B28551.
InterPro; IPR003469; Glyco_hydro_68.
Pfam; PF02435; Glyco_hydro_68; 1.
Transferase; Glycosyltransferase; Signal.
                                                                                                                               YFAL_ECOLI
NFM_CHICK
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MAP2_HUMAN
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MEDLINE=88115184; PubMed=2828325;
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797 AA; 87574 MW;
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SEQUENCE FROM N.A.
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NCBI_TaxID=1309;
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P11701;
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                                                                              September 26, 2002, 18:23:41; Search time 22.4 Seconds (without alignments) 1363.827 Million cell updates/sec
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P0555 bacillus su
P21130 bacillus su
P21130 bacillus su
G60115 zymomonas m
Q66115 zymomonas m
Q4654 erwinia amy
O54435 rahnella aq
O54398 acetobacter
P14738 staphylococ
P27951 streptococc
P16952 streptococc
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P165443 streptococc
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1 MYKSGKNWAVVTLSTAALVF.....GMGTLLSMFGLAEINKRFFN 789
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P21979
P52143
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                           Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                      105224 seqs, 38719550 residues
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    protein search, using sw model

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Maximum Match 100%
Listing first 45 summaries
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SACE_BACSU
SACE_BACSU
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Match Length D
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STRAIN-ATCC 25975;
WHEDLINE-9332232: PubMed-8331080;
Rathsam C., Giffard P.M., Jacques N.A.;
"The cell-bound fructosyltransferase of Streptococcus salivarius: the carboxyl terminus specifies attachment in a Streptococcus gordonii
SELAERSQVQENTTASSSAAENQAKTEVQET------PSTNPAAATVENTDQTTKVIT
                    ENTINTAKNDDTQKAAPANESSEAKNEPAV---NVNDSSAAKNDDQQSSKKNTTAK--LNK
                                                             DAENVVKKAGIDPNSLTDDQIKALNKMNFSKAAKSGTQMTYNDFQKIADTLIKQDGRYTV
                                                                         233 PFFKASEIKNMPAATTKDAQTNTIEPLDVWDSWPVQDVRTGQVANWNGYQLVIAMMGIPN
                                                                                                                                                QNDNHIYLLYNKYGDNELSHWKNVGPIFGYNSTAVSQEWSGSAVLNSDNSIQLFYTRVDT
                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                                                                                                                                                                             IKSRATWANAAIGILKLNKDEKNPKVAELYSPLISAPMVSDEIERPNVVKLGNKYYLFAA
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                                                                                                                                                                                                                                                                                                                                    SYYAVPVAGKDDQVLVTSYMTNRNGVAGKGMDSTWAPSFLLQINPDNTTTVLAKMTNQGD
                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Levansucrase precursor (EC 2.4.1.10) (Beta D-fructofuranosy)
transferase) (Sucrose 6-fructosyl transferase).
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NCBI_TaxID=1304;
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Q55242;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                           18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 TNHQKIASATLYLTDNNGNVSLAQVRNDYIVFEGDGYYYQTYDQWKAT----NKG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFAATRLNRGSNDDAMMNANYAVGDNVAMVGYVADSLTGSYKPLNDSGVVLTASVPANWR
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                                                                                                                                                                                                                                                                                                                        75;
                                                                                                                                                                                                                                                                                                 Length 969;
J. Bacteriol. 175:4520-4527(1993).
-!-CATALTIC ACTULTY: SUCROSE + (2.6-BETA-D-FRUCTOSYL)(N)
GLUCOSE + (2.6-BETA-D-FRUCTOSYL)(N+1) (OTHER SUGARS CAN
ALSO ACT AS FRUCTOSYL ACCEPTORS).
-!-SUBCELLULAR LOCATION: SECRETED. CELL-WALL BOUND.
-!-SUBCELLULAR ELCONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                      Llarity 45.7%; Pred. No. 2e-79;
Conservative 135; Mismatches 227; Indels
                                                                                                                                                                                                                                             LEVANSUCRASE.
                                                                                                                                                                  42.1%; Score 1739.5; DB 1; 45.7%; Pred. No. 2e-79;
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103983 MW;
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Best Local Simi:
Matches 368; (
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696 -------PNDPETPTTPETPETPNTPKTPRTPENPCT--PQTPNTPNTPEIP 738
                                                  739 HGVLTVTVKDGKDKKADKPETPVSPTEGNHSVDDKTNK----PGTSKPADNNQPSADKED 794
                                                                                                                                                                                                                                                                                                                       STRAIN=168;
MEDLINE-85295507; PubMed-2993818;
Steinmetz M., Le Coq D., Aymerich S., Gonzy-Treboul G., Gay P.;
The DNA sequence of the gene for the secreted Bacillus subtilis enzyme levansucrase and its genetic control sites.";
Mol. Gen. Genet. 200:220-228(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-87008406; PubMed=2428811;
Shinotsu H., Henner D.J.;
"Modulation of Bacillus subtilis levansucrase gene expression by
sucrose and regulation of the steady-state mRNA level by sacU and
                                                                                                                                                                     01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
Levansucrase precursor (EC 2.4.1.10) (Beta-D-fructofuranosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fouet A., Arnaud M., Klier A., Rapoport G.; "Characterization of the precursor form of the exocellular levansucrase from Bacillus subtilis."; Blochem. Blophys. Res. Commun. 119:795-800(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                   Denizot F.C.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                  Bacteria, Firmicutes, Bacillus/Clostridium group;
Bacillus/Staphylococcus group, Bacillus.
                                                                                                                                                                   473 AA.
                                                                                                                                                                   PRT;
                                                                              739 LTPETPKQPETQTNNRLPQTGNNAN 763
                                                                                                   795 -KPTNPTNPDSPARTPFPYYGDHSN 818
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MEDLINE-84178454; PubMed-6424671;
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EMBL; K01987; AAA22724.1;
EMBL; X02730; CAA26513.1;
EMBL; 299121; CAB15450.1;
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                                                                                                                                                                 STANDARD;
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226 QDGRYTVPFFKASEIKNMPAATTKDAQTNTIEPLDVWDSWPVQDVRTGQVANWNGYQLVI 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          453 GDDAFNIKSLFRILSNDDIKSRATWANAAIGILKLNKDEKNPKVAELYSPLISAPMYSDE
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MEDLINE=91092506; PubMed=2265762;
Tang L.B., Lenstra R., Borchert T.V., Vasantha N.;
"Isolation and characterization of levansucrase-encoding gene from
                                                                                                                                                                                                     16;
       PIR; S07309; S07309.
Subthist; BG10388; sacB.
Subthist; BG10388; sacB.
Pfant: PR003469; Glyco_hydro_68.
Transferase; Glycosyltransferase; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Levansucrase precursor (EC 2.4.1.10) (Beta-D-fructofuranosyl transferase) (Sucrose 6-fructosyl transferase).
                                                                                                                                                                         Length 473;
                                                                                                                                                                  Score 744; DB 1; Length 47;
Pred. No. 2.4e-30;
7; Mismatches 151; Indels
                                                                                           30 473 LEVANSUCRASE.
12 12 V -> I (IN REF. 3).
473 AA; 52971 MW; 3FBF2F5571B41D5B0 CRC64;
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Matches 183; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKGKKTSVVKDSILEQG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus amyloliquefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
A25040; A25040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=ATCC 23844;
                                                                                                        CONFLICT
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P21130;
                                                                                                                                                               Query Match
Best Local S
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CHAIN
SEQUENCE
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                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is not its modified and this statement is not removed. Usage by an order in the order is not removed. Its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 ENVYKKAGI---DPNSLTDDQIKALNKMNFSKAAKSG---TQMTYNDFQKIADTLIKQDG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 RYTVPFFKASEIKNMPAATTKDAQTNTIEPLDVWDSWPVQDVKTGQVANMNGYQLVIAMM 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 SDNSIQLEYTRVDTSDNNTNHOKIASATLYLTDNNGNVSLAQVRNDYIVFEGDGYXXQTY 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOW--KATNKGADNIAMRDAHVIEDGNGDRYLVFEASTGLEN-YQCEDQIYNWLNYGGDD 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            + KKIVKQATVLTFTTALLAGGATQAFAKENNOKAYKETYGVSHITRHDMLQIPKO--QQNE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           516 PNVVKLGNKYYLFAATRLNRGSNDDAWMNANYAVGDNVAMVGYVADSLTGSYKPLNDSGV 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      576 VLTASVPANNRTATYSYXAVPVAGKDDQVLVTSYMTNRNGVAGKGMDSTWAPSFLLQINP 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 GIP-NQNDNHIYLLYNKYGDNELSHWKNVGPI-----FGYNSTAV---SQEWSGSAVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   456 AFNIKSLFRILSNDDIKSRATWANAAIGILKLNKDEKNPKVAELYSPLISAPMVSDEIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
Bacillus amyloliquefaciens.";
Gene 96:89-93(1990).
-!-CATALTIC ACTIVITY: SUCROSE + (2,6-BETA-D-FRUCTOSYL)(N) -
GLUCOSE + (2,6-BETA-D-FRUCTOSYL)(N+1) (OTHER SUGARS CAN
ALSO ACT AS FRUCTOSYL ACCEPTORS).
-!-SUBCELLULAR LOCATION: Secreted.
-!-INDUCTION: BY SUCROSE.
-!-SIMILARITY: BELONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.0%; Score 741.5; DB 1; Length 472; 38.1%; Pred. No. 3.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEVANSUCRASE.
F38592D272677E7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,1e-30;
                                                                                                                                                                                                                                                                                                                                                                                      Pirk; Sil739; Sil739.
Interpro; IRO03469; Glyco_hydro_68.
Pfam; PF02435; Glyco_hydro_68; I.
Transferase; Glycosyltransferase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 472 LF
472 AA; 52859 MW;
                                                                                                                                                                                                                                                                                                                                    EMBL; X52988; CAA37179.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           454 NKTSVVKNSILEQG 467
                                                                                                                                                                                                                                                                                                                                                            PIR; JQ0802; JQ0802
PIR; S11739; S11739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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P94468;
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SACB_BACST
  $\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\f
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473 AA.

PRT;

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396 QTYDQW--KATNKGADNIAMRDAHVIEDGNGDRYLVFEASTGLEN-YQGEDQIYNWLNYG 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           453 GDDAFNIKSLFRILSNDDIKSR-ATWANAAIGILKLNKDEKNPKVAELYSPLISAPMVSD 511
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Levansucrase precursor (EC 2.4.1.10) (Beta-D-fructofuranosyl transferase) (Sucrose 6-fructosyl transferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li Y., Triccas J.A., Ferenci T.;
"A novel levansucrase-levanase gene cluster in Bacillus stearchtermophilus ATCC12980.";
"I caralytic Acta 1353:203-208(1997).
"I CATALYTIC ACTYLITY: SUGROSE + (2,6-BETA-D-FRUCTOSYL)(N) = GLUGOSE + (2,6-BETA-D-FRUCTOSYL)(N+1) (OTHER SUGARS CAN ALSO ACT AS FRUCTOSYL SCREPCORS).
"I SUBCELLUIAR LOCATION: Secreted.
"I SIMILARITY: BELONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 473;
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36.3%; Pred. No. 3.38-29;
tive 90; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEVANSUCRASE.
12F7A272EC2B771E CRC64;
                                                                                                                                                                                                                                                   Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/staphylococcus group; Geobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Difference, proposed and proposed by the propo
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-ATCC 12980;
MEDLINE-98007870; Pubmed-9349714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 MNFSKAAKSGTQMTY------
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Matches 181; Conservative
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             572 DSGVVLTASVPANWRTATYSYYAVPVAGKDDQVLVTSYMTNRNGVAGKGMDSTWAPSFLL 631
                                                                                                                                                                                                                                                                                                                                           Song K.B., Joo H.K., Rhee S.-K.;
Nucleotide sequence of levansucrase gene (levU) of Zymomonas mobilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kyono K., Yanase H., Tonomura K., Kawasaki H., Sakai T.; "Cloning and characterization of Zymomonas mobilis genes encoding extracellular levansucrase and invertase."; Blotechnol. Blochem. 59:289-293(1995).
                                                                                                                                  SACH_ZYMMO STANDARD; PRT; 423 AA.

560114; 060116; 006487;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last Sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-Varnsucrase (EC 2.4.1.10) (Beta-D-fructofuranosyl transferase)
5ACE OR LEVU OR SUCE2.
                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, alpha subdivision; Sphingomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-NRRL B806;
Gunasekaran P., Mukundan G., Kannan R., Velmurugan S.,
Alt-Abdelkader N., Alvarez E., Baratti J.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                               Biochim. Blophys. Acta 1173:320-324(1993).
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-IFO 13756;
MEDLINE-95218269; Pubmed-7766026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF313764; AAG29870.1; -InterPro; IPR003469; Glyco,hydro_68. Pfam; PF02435; Glyco_hydro_68; 1. Transferase; Glycosyltransferase.
                                                                                                                                                                                                                                                                                                                            MEDLINE-93305726; PubMed-8318541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-AICC 31821 / ZM4 / CP4;
                                               632 QINPDNTTTVLAKMTNQG 649
                                                                        450 NIOGKKTSVVKASILDOG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF081588; AAA27695.1; -.
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                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-ATCC 10988 / ZM1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                   250 DAQTNIIEPLD-----GIPN 292
                                                                                                                                             Gaps
                                                                                                                                                                                               293 QNDN-HIYLLYNKYGDNELSHWKNVGPIFGYNSTAVSQEWSGSAVL--NSDNSIQLFYTR 349
                                                                                                                                                                                                                VDTSDNNTNHQKI-ASATLYLTDNNGNVSLAQVRNDYIVFEGDGYYYQTYDQWKATNKGA 408
                                                                                                                                                                                                                                                                   139 V----NDTPSESVPAQCKGYIYADDKSVWFDGFDKVTDLFQADGLYYADY----AENNFW 190
                                                                                                                                                                 409 DNIAMRDAHV-IEDGNGDRYLVFEASTGLENYQGEDQIYNWLNYGGDDAFNIKSLFRILS 467
                                                                                                                                                                                                                                                                                                                                                                                                      582 PANWRTATYSYYAVPVAGKDDOVLVTSYMTN-----RNGVAGKGMDSTWAPSFLLG 632
                                                                                                                                                                                                                                                                                                          468 NDDIKSRATWANAAIGILK-LNKDEKNPKVAELYSPLISAPMVSDEIERPNVVKLGNKYY
                                                                                                                                                                                                                                                                                                                                                              234 KTETPDGARYCAAAIGIAQALNEARTEWK----LLPPLVTAFGVNDQTERPHVVFONGLTY
                                                                                                                                                                                                                                                                                                                                                                                      LFAATRLNRGSNDDARMNANYAVG----DNVAMVGYVADS-LTGSYKPLNDSGVVLTASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 PSSOPYQAYSHYVM-----TNGLVTSFIDTIPSSDPNVYRYG------GTLAPTIKLE
                                                                                                         7.4%; Score 304; DB 1; Length 423;
26.6%; Pred. No. 1.5e-08;
Live 74; Mismatches 155; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of an extracellular
(ATCC10988).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zymomonas mobilis.
Zymomonas mobilis.
Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
          1F. 2).
(IN REF. 1 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INVB_ZYMMO STANDARD; PRT; 413 AA.

15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Extracellular sucrase (EC 3.2.1.26) (Beta-fructofuranosidase)
SACC OR INVB OR SUCES.
     V -> I (IN REF. 2).

NPED -> TPKI (IN REF. 1 AND E -> Q (IN REF. 2).

T -> A (IN REF. 2).

C -> Y (IN REF. 2).

I -> V (IN REF. 2).

M. 1944691DA3EB9FE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
STRAIN-IFO 13756;
MEDLINE-95218269; PubMed-7766026;
Kyono K., Yanase H., Tonomura K., Kawasaki H., Sakai T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Song K.B., Lee S.K., Joo H.K., Rhee S.-K.;
"Nucleotide and derived amino acid sequences sucrase gene (invB) of zymomonas mobilis ZM Biochim. Biophys. Acta 1219:163-166(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               633 INPDNTTTVLAK----MINQGDWIWDDSSEN 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 LVGHRSFVTEVKGYGYIPPQIEWLAEDESSN 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-ATCC 10988 / ZM1;
MEDLINE-94368848; Pubmed-8086457;
   39 V
203 NI
217 E
220 T
244 C
379 I
                                                                                                                                 Conservative
   39
200
217
220
244
379
423 AA;
                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=542;
                                                                                                                   Best Local Sin
Matches 120;
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                      Query Match
                                                                                                                                                                                                                        83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                     MEDLINE-95297907; Pubmed-7778976;
Kannan R., Mukundan G., Alt-Abdelkader N., Augier-Magro V.,
Baratti J., Gunasekaran P.;
"Molecular cloning and characterization of the extracellular sucrase
                                                                                                                                                                               257 EPLDVWDSMPVQDVRTGQVA--NWNGYQLVIAMMGIPNQNDNH----IYLLXNKYGDNEL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     characterization of Zymomonas mobilis genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                           G -> A (IN REF. 3).
T -> S (IN REF. 2).
T -> S (IN REF. 2).
PVWP -> LGMA (IN REF. 3).
W: BACC12D167332E47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.3%; Score 301.5; DB 1;
26.8%; Pred. No. 2e-08;
.1ve 79; Mismatches 141;
                extracellular levansucrase and invertase ";
Blosci. Biotechnol. Biochem. 59:289-293(1995).
                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF313764; AAG29871.1;
InterPro; IPR003469; Glycc_hydro_68.
Pfam; PF02435; Glycc_hydro_68; 1.
                                                                                                                     gene (sacC) of Zymomonas mobilis."; Arch. Microbiol. 163:195-204(1995).
           extracellular levansucrase and
                                                                                                                                                                         / ZM4 / CP4;
                                                                                                                                                                                                                                                                                                                                                   EMBL; AF081588; AAA61488.1; -
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                                                                                                                                                                                                                                                                                                                                                                                   AAC36942.1; -.
                                                                                                                                                                                                                                                                                                                                                                  D17524; BAA04476.1;
L33403; AAC36942.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                Glycosidase
                                                                                                                                               [4]
SEQUENCE FROM N.A.
                                                                                                                                                                     STRAIN-ATCC 31821
                                                                                                                                                                                                                                                                                                                                                                                                                                                    105
108
404
413 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al Similarity
108: Conserv
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Hydrolase; C
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Matches
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525 YYLFAATRLNRGSNDDAWMNANYAVGDNV----AMVGYVADSLTGSYKPLNDSGVVLTAS
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311 SHWKNVGPIFGYNSTAVSQEWSGSAVL--NSDNSIQLFYTRVDTSDNNTNHQKIASAT-- 366
              367 -LYLTDNNGNVSLAQVRNDYIVFEGDGYYYQTYDQWKATNKGADNIAMRDAHV-IEDGNG 424
                                                                                                    DRYLVFEASTGLENYQGEDQIYNWLNYGGDDAFNIKSLFRILSNDDIKSRATWANAAIGI 484
                                                                                                                              485 LKLNKDEKNPKVAELYSPLISAPMVSDEIERPNVVKLGNKYYLFAATRLNRGSNDDAWMN 544
                                                             152 RIY - ADSEG-VWFKGFDQSTDLFQADGLFYQNYAENNLWN-----FRDPHVFINPEDG
                                                                                                                                                                          ANYAVG--DNVAMVGYVADS-LTGSYKPLNDSGVVLTASVPANWRTATYSYYAVPVAGKD
                                                                                                                                                   ARCLSPDRTE--WELLPPLLTAFGVNDOMERPHVIFQNGLTYLFTISH-----D
                                                                                                                                                                                        602 DQVLVTSYMTN----RNG--VAGKGMDSTWAPSFLLQINPDNT 638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 EPLDVWDSWPVQDVRTGQVANWNGYQLVIAMMGIPN-----QNDNHIYLL----YNKYG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137; Indels 106; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 DNELSHW-KNVGP--IFGYNSTA----VSQEWSGSAV-LNSDNSIQLFYTRVDTSDNNT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NHQKIASATLYLTDNNGNVSLAQVRNDYIVFBGDGYYYQTYDQ---WKATNKGADNIAMR 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415 D-AHVIEDGNGDRYLVFEASTGLENYQGEDQIY-----NMLNYGGDDAFNIKSLFR 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86
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40 EEVFINDIMPLRDF-DGEIISVNGWCIIFTLTADRNTDNPQFQDENGNYDITRDWEDRHG
                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Levansucrase (EC 2.4.1.10) (Beta-D-fructofuranosyl transferase)
(Sucrose 6-fructosyl transferase).
                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    465 ILSNDDIKSRATWANAAIGILKLNKDEKNPKVAELYSPLISAPMVSDEIERPNYVKLGNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | : |: :| |::|| : :| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 281; DB 1; Length 415;
Pred. No. 2.1e-07;
3; Mismatches 137; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003469; Glyco_hydro_68.
Pfam; PF02435; Glyco_hydro_68; 1.
Transferase; Glycosyltransferase.
SEQUENCE 415 AA; 46408 MW; 4FF564F6E0607FEB CRC64;
348 NNGLVESFINEIIDPKSGKVIAGGSL----APTVRVELQGHET 386
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                                                                                                                                                                     415
                                                                                                                                                                  PRT;
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25.6%; Pred
73; )
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                                                                                                                                                      STANDARD;
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Best Local Similarity 25.6%
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                      Erwinia amylovora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=552;
                                                                                                                                               SACB_ERWAM
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                                                                                     RESULT 8
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22;

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SACB_PSESH
O68609;
                                                                                                                  306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EWBL outstation use by non-profit institutions as long as its content is in no its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
581 VPANWRTATYSYYAVPVAGKDDQVLVTSYMTNRNGVAGKGMD----STWAPSFLLGINPD 636
                            310 LSHWKN-----VGPIFGYNSTAVSOEWSGSAV-LNSDNSIQLFYTRVDTSDNNTNHQ 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LYNKYGDNE 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 KIASATLYLTDNNGNVSLAQVRNDYIVFEGDGYYYQTYDQ---WKATNKGADNIAMRD-A 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 TIAKVRGKVLTSEEGVTLAGFNEVKSLFSADGVYYQTESQNPYWN-----FRDPS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |: :| |:||| : | | |
PFIDPHDGKLYMVFEGNVAGE--RGSHVI-----GKQEMGTLPPGHRDVGN-----AR 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HVIEDGNGDRYLVFEASTGLENYQGEDQIYNWLNYGGDDAFNIKSLFRILSNDDIKSRAT 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                477 WANAAIGIL---KLNKDEKNPKVAELYSPLISAPMVSDEIERPNVVKLGNKYYLFAATRL 533
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

C STRAIN-ATCC 33071;
X MEDLINE-9127094; PubMed-9928133;
A SONG K.B., Seo J.W., Kim M.C., Rhee S.K.;
T.Eevansucrase of Rahnella aquatilis ATCC33071. Gene cloning, T. T. Ann. N.Y. Acad. Sci. 864:506-511(1998).
C I- CATALYTIC ACTIVITY: SUCROSE + (2.6-BETA-D-FRUCTOSYL)(N) = (5.6-BETA-D-FRUCTOSYL)(N) = (5.6-BETA-D-FRUCTOS
                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Levansucrase (EC 2.4.1.10) (Beta-D-fructofuranosyl transferase)
(Sucrose 6-fructosyl transferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR003469; Glyco_hydro_68.
Pfam; PF02435; Glyco_hydro_68; 1.
Transferase; Glycosyltransferase.
SEQUENCE 415 AA; 45939 MW; E028828813D13A74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1: 11::1 1:1: 111: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.7%; Score 275.5; DB 1;
27.2%; Pred. No. 3.9e-07;
tive 58; Mismatches 132;
                                                                                                                                                                                                                       415 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 VWDSWPVQDVRTGQVANWNGYQLVIAMMGIPNQNDNHIYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U91484; AAC36458.1; -.
                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                         Rahnella aquatilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 104; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=34038;
                                                                        637 NTTTV 641
                                                                                                              394 RSFIV 398
                                                                                                                                                                                                          SACB_RAHAO
054435:
                                                                                                                                                                  RESULT 9
SACB_RAHAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRAIN-NOPPB 1321;
RX MEDLINE-98394981; Pubmed-9726857;
RA HETEWER U., Jaeckel F.R., Boch J., Meyer M., Rudolph K., Ullrich M.S.;
RT "Cloning, nucleotide sequence, and expression in Escherichia coli of
RT glycinea and P. syringae pv. phaseolicola."
RL Appl. Environ. Microbiol. 64:3180-3187(1998)
C. - CATALYTIC ACTIVITY: SUCROSE + (2.6-BETA-D-FRUCTOSYL)(N) -
ALSO ACT AS FRUCTOSYL ACCEPTORS)
C. - SUBCELLULAR LOCATION: Secreted.
C. - SUBCELLULAR LOCATION: Secreted.
C. - SIMILARITY: BELONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES.
C. - SIMILARITY: BELONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
252 YQAGCIGMAVAKDLSGDE-----WEILPPLVTAVGVNDQTERPHFVFQDGKYYLFTISH- 305
                                             534 NRGSNDDAWMNANYAVG----DNVAMVGYVADSLTGSYKPLNDSGVVLTASVPANWRTAT 589
                                                                                238 SEIKNMP-----DVWDSWPVQD 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----VGPIFGYNSTAVSQEWSGSAV-LNSDNSIQLFYTRVDTSDNNTNHQKIASATLYL 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 TDNNGNVSLAQVRNDYIVFEGDGYYYQTYDQWKATNKGADNIAMRD-AHVIEDGNGDRYL 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68
                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Levansucrase (EC 2.4.1.10) (Beta-D-fructofuranosyl transferase)
(Sucrose 6-fructosyl transferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 SQLKNISPLAGNINYEPTVWSRADALKVNENDPTTTOPLVSADFPVWSDTVFIWDTMPLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 VRTGQVANWNGYQLVIAMKGIPNQNDNHIYLLYN-------KYGDNELSHWKN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas syringae (pv. phaseolicola).
Bacteria, Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 274; DB 1; Length 431;
; Pred. No. 4.8e-07;
66; Mismatches 165; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF052289; AAC36063.1; -
InterPro; IPR003469; Glyco_hydro_68.
Pfam; PF03435; Glyco_hydro_68; 1.
Transferase; Glycosyltransferase.
SEQUENCE 431 AA; 47603 MW; 795FEA246D40C40F CRC64;
                                                                                                                                                                                                                                                                                                                           431 AA.
                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                        590 YSYYAVPVAGKDDQVLVTSYMTN 612
                                                                                                                                                                        352 YSHCVMP-----NGLVTSFIDN 368
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Best Local Similarity 25.19
Matches 115, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=319;
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15-DEC-1998 (
15-DEC-1998 (
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181 VTSDQGVELKDFTQVKKLFEADGTYYQTEAQNSSWN-----FRDPSPFIDPNDGKLYM 233
                                                         429 VFEASTGLENYGGEDQIYNWLNYGGDDAFNIKSLFRILSNDDIKSRATWANAAIGILKLN 488
                                                                                                             234 VFEG-----NVAGE-----RGSHTVGAAELGPVPPGHEDVGGARFQVGCIG-LAVA 278
                                                                                                                                                                      489 KDEKNPKVAELYSPLISAPMYSDEIERPNVVKLGNKYYLFAATRLNRGSNDDAMMNANYA 548
                                                                                                                                                                                                        Arrieta J., Hernandez L., Coego A., Suarez V., Balmori E., Menendez C., Petit-Glatron M.-F., Chambert R., Selman-Housein G.; "Molecular characterization of the levansucrase gene from the endophytic sugarcane bacterium Acetobacter diazotrophicus SRT4.";
-I-FUNCTION: RELEASES FRUCTOOLIGOSACCHARIDES AND LEVAN, A HIGH-NOLECULAR-MASS FRUCTOSYL POLYMER, FROM SUGROSE. IT ACTS MORE AS SUCROSE HYDROLASE TRAIN AS A FRUCTAN POLYMERASE.
-I-CAPALYTIA ACTIVITY: SUCROSE + (2,6-BETA-D-FRUCTOSYL)(N) - GLUCOSE + (2,6-BETA-D-FRUCTOSYL)(N) - CAPALYTIA CATIVITY: SUCROSE HYDROLASE CAN ASSECTION OF A COMMENT OF A COMME
                                                                                                                                                                                                                                                                                   549 VG----DNVAMVGYVADSLTGSYRPLNDSGVVLTASVPANWRTATYSYXAVPVAGKDDQV
                                                                                                                                                                                                                                                                                                                     Acetobacter diazotrophicus (Gluconacetobacter diazotrophicus).
Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
Gluconacetobacter.
NCBI_TaxID=33996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Levansucrase precursor (EC 2.4.1.10) (Beta-D-fructofuranosyl transferase) (Sucrose 6-fructosyl transferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALSO ACT AS FRUCTOSYL ACCEPTORS)

1 SUBCELLUIAR LOCATION: Secreted

1- PTW. THE N-TERMINAL IS BLOCKED.

1- SIMILARITY: BELONGS TO FAMILY 68 OF GIYCOSYL HYDROLASES.
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                                                                                                                                                                                                                                                                                                                                                                                                605 LVTSYMTNRNGVAGKGMD----STWAPSFLLQINPDNT 638
                                                                                                                                                                                                                                                                                                                                                                                                                                     584 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 52-61.
STRAIN-SRT4 / CBS 550.94;
MEDLINE-96253999; PubMed-8704949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003469; Glyco_hydro_68
Pfam; PF02435; Glyco_hydro_68; 1.
Transferase; Glycosyltransferase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEVANSUCRASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         584 AA;
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Q43998;
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SEQUENCE
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209 TQMTY---NDFQ----KIADTL-IKQDGRYTVPFFKASBIKNMPAATTK---DAQTNTIEP 258
                                                       74 TQQAYDPQSDFTARWTRADALQIKAHSDATV----AAGQNSLPAQLTMPNIPADFPVINP 129
                                                                                                                                                                                                                                                                  LSH-----WKNYGPIFGYNSTAV-----SQEWSGSAVLNS--DNSIQLFYTRV--- 350
                                                                                                                                                                                                                                                                                                                             189 SRRPVNGGWTYGGHLFPDGASAQVYAGQTYTNQAEWSGSSRLWQIHGNTVSVFYTDVAFN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hettwer U., Jaeckel F.R., Boch J., Meyer M., Rudolph K., Ullrich M.S.;
"Cloning, nucleotide sequence, and expression in Escherichia coli of
levansucrase genes from the plant pathogens Pseudomonas syringae pv.
Appl. Environ. Microbiol. 64:3180-3187(1998).
- CATALTITIC SATIVITY: SUCROSE + (2,6-BETA-D-FRUCTOSYL)(N) =
ALSO ACT AS FRUCTOSYL (M+1) (OTHER SUGARS CAN
ALSO ACT AS FRUCTOSYL ACCEPTORS).
- SUBCELLOLAR LOCATION: Secreted.
- SIMILARITY: BELONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYDQWKATNKGADN--IAMRDAHVIEDGN--GDRYLVFEAST----GLENYQGEDQIYNW 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   449 LNYGGDDAFNIKSLFRILSNDDIKSRATWANAAIGILKLNKDEKNPKVAELYSPLISAPM 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 565 GSYRPLNDSGVVLTASVPANWRTA------TYSYYAVPVAGKDDQVLVT 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 443 SDFQPMN-YGSGLTMGNPTDLNTAAGTDFDPSPDQNPRAFQSYSHYVMPGG-----LVE 495
                                                                                                                                 -LDVWDSWPVQDVRTGQVANWNGYQLVIAMMGIPNQ----NDNHIY----LLYNKYGDNE
                                                                                                                                                                                                                                                                                                                                                                                            351 -DTSDNN-TNHQKIASATLYLTDNNGNVSLAQVRNDY--IVFEG-------------DGYYYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                         : |||:| : | | ::||:::: | | :|| ::|| : | | :|| :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| 
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Levansucrase (EC 2.4.1.10) (Beta-D-fructofuranosyl transferase)
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Bacteria, Proteobacteria, gamma subdivision, Pseudomonadaceae,
Pseudomonas
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MEDLINE=98394981; PubMed=9726857;
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O52408;
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35;

Gaps

6.4%; Score 266; DB 1; Length 584; 26.9%; Pred. No. 1.8e-06; Live 63; Mismatches 171; Indels 150;

Query Match Best Local Similarity 26.9 Matches 141; Conservative

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Query Match
Best Local S
Matches 195
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X MEDILINE-8908998; PubMed-2521391;

A Signaes C., Raucci G., Densson K., Lindgren P.-E.,

Anantharamaiah G.M., Hoeoek M., Lindberg M.;

I "Nucleotide sequence of the gene for a fibronectin-binding protein

T row Staphylococcus aureus: use of this peptide sequence in the

T synthesis of biologically active peptides.

T synthesis of biologically active peptides.

T refunction: THE ABILITY OF BACTERIA TO BIND FIBRONECTIN HAS BEEN

WONND TISSUES AND BLOOD CLOTS. BINDING OF PLASHA FIBRONECTIN

THE BACTERIAL SURFACE MIGHT BLOCK ADHESION RECEPTORS ON S.AUREUS.

THE BACTERIAL SURFACE MIGHT BLOCK ADHESION RECEPTORS ON S.AUREUS.
                                                                                                                                          261 VWDSWPVQDVRTGQVANWNGYQLVIAMMGIPNQND-----NHIYLL----YNKYGDNEL 310
                                                                                                                                                         SHWKN------VGPIFGYNSTAVSQEWSGSAV-LNSDNSIQLFYTRVDTSDNNTNHQK 361
                                                                                                                                                                                                  362 IASATLYLTDNNGNVSLAQVRNDYIVFEGDGYYYQTYDQWKATNKGADNIAMRD-AHVIE 420
                                                                                                                                                                                                                                                     157 IAKVRGRIVTSDKGVELKDFTEVKTLFEADGKYYQTEAQNSTWN-----FRDPSPFID 209
                                                                                                                                                                                                                                                                            421 DGNGDRYLVFEASTGLENYQGEDQIYNWLNYGGDDAFNIKSLFRILSNDDIKSRATWANA 480
                                                                                                                                                                                                                                                                                                 210 PNDGKLYMVFEG-----NVAGE------RCTHTVGAAELGPVPPGHEETGGARFOVG 255
                                                                                                                                                                                                                                                                                                                                     537
                                                                                                                                                                                                                                                                                                                                                           302
                                                                                                                                                                                                                                                                                                                                                                               303 ----ISHKFTYADGVTGPDGVYGFVGEHLFGPYRPMNASGLVL-GNPPAQ-PPQTYSHC 355
                                                                                                                                                                                                                                                                                                                      481 AIGIL---KLNKDEKNPKVAELYSPLISAPMVSDEIERPNVVKLGNKYYLFAATRLNRGS
                                                                                                                                                                                                                                                                                                                                      538 NDDAWMNANYAVGDNV----AMVGYVADSLTGSYKPLNDSGVVLTASVPANWRTATYSYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Type I membrane protein. Cell wall. SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS
                                                                                                                                 88;
                                                                                                          Length 415;
                                                                                                   6.2%; Score 257; DB 1; Length 41
25.2%; Pred. No. 3.2e-06;
ive 66; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             594 AVPVAGKDDQVLVTSYMTNRNGVAGKGMD----STWAPSFLLQINPDNT 638
                                                                                                                                                                                                                                                                                                                                                                                                                             839B686AC80610CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus.
Bacteria: Firmicutes: Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR'1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Fibronectin-binding protein precursor (FNBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1018 AA
   to license@isb-sib.ch).
                 EMBL; AF037443; AAC36056.1; -... InterPro; IPR003469; Glyco_hydro_68.Pfam; PF02435; Glyco_hydro_68; Iransferase; Glycosyltransferase; SEQUENCE 415 AA; 45844 MW; 839B6
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : STANDARD;
                                                                                                            Similarity
   ema11
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SEQUENCE FROM N.A.
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Matches 103;
   an
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P14738;
                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 AASLANTDSKAAQENTNTAK--NDDTQKAAPANESSEAKNEPAVNVNDSSAAKNDDQQSS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTLGSGQVSAASD---TTIRTSANANSASSAANTQNSNSQV-----ASSAAITSSTSS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 VGMGQDKEAAASEQKTTTVEENGNSATDNKTSETQTTATNVNHIEETQSYNATVTEQPSN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 TVEIGSIEGHNNTNKVEPHAGQRAVLKYKLKFENGLHQGDYFDFTLSNNVNTHGVSTARK 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 ASEIKN------MPAATTKDAQTNTIE-PLDVWDSWPVQ---DVRTGQVANWNGYQ 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283 LVIAMM------GIPN--QNDNHIYLLYNKYGDNELSHWKNVGPIFGYNS- 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 TITSTLNEEQTSKELDVKYKDGIGNYYANLNGSIETENK-ANNRESHVAFIKPNNGKTTS 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      378 VTVTGTLMKGSNQNGNQPKVRIFEYLGNNEDIAKSVYANTTDTSKFKEVTSNMSGNLNLQ 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 KKNTTAKLNKDAENVVKKAGIDPNSLTDDQIKALNKMNFSKA-----AKSGTQMT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 -----YNDFQKIAD----TLIK----QDGRYTVPFF-----K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 VPEIKNGSVVMATGEVLEGGKIRYTFTNDIEDKVDVTAELEINLFIDPKTVQT---NGNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -TAVSQEMSGSAVLNSDNSIQLFYTRVDTSD-----NNTNHQKIASATLYLT----D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INCOMPLETE).
TANDEM REPEATS, PRO-RICH (WR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 255; DB 1; Length 1018;
Pred. No. 1.3e-05;
5; Mismatches 322; Indels 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEATS,
                                                                                                                                                                                                                                                                                                                                                  FIBRONECTIN-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 X APPROXIMATE TANDEM REPE
FIBRONECTIN-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58175E0020E81F1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                   EMBL; J04151; AAA26632.1;
InterPro; IPR004237; Fn_bind.
InterPro; PR004237; Fn_bind.
Pfam; PF02286; Fn_bind; 1.
Pfam; PF00746; Gram_pos_anchor; 1.
Signal; Repeat; Cell Wall; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity 18.4%; Pre 195; Conservative 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.2%;
                                                                                                                                                                                                                                                                                                                                                              993
1009
1018
574
604
878
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948
892
906
920
934
948
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DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELULAR (POTENTIAL).
MEMBRANE ANCHOR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
IG-LIKE DOMAIN.
IGA-BINDING (POTENTIAL).
IGA-BINDING (POTENTIAL).
PRO-RICH REPEATS.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
5.8%; Score 241; DB 1; Length 1164;
Best Local Similarity 20.0%; Pred. No. 7.8e-05;
Matches 191; Conservative 130; Mismatches 347; Indels 288; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 ---KAAPANESSEAK---NEPAVNVNDSSAAKNDD-----QQSSKK------ 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 LNHQKSQVEKMAEQKGITNED----KDSMLKKIEDIRKQAQQADKKEDAEVKVREELGKL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 VVTLSTAALVFGA-----VQV 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --NTTAKLNKDAENVVKK-----AGID---PNSLTDDQIKALNKMNFSKAAKSGTQM 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 FSSTRAGLDQEIQEHVKKETSSEENTQKVDEHYANSLQNLAQKSLEELDKATTNEQATQV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 TYNDF----OKIAD--TLIKQDGRYTVPFFKA-----SEIKNMPAATTKDAQTNTI 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 VASVAVASLFMGSVAHASELVKDDSVKTTEVAAKPYPSMAQTDQGNNSSSSELETTKMEI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 TTGDNDIAVKSVTLGSGQVSAASDTTIRTSA----NANSASSAANTQNSNSQVASSAAIT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 K-NOFLENAQKLKEIQPLIKET---NVKLYKAMSESLEQVEKELKHNSEANLEDLVAKSK 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257 EPLDVWDS-----WPVQDVRTGQVAN 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            370 EIVREYEGKLNQSKNLPELKQLEEEAHSKLKQVVEDFRKKFKTSEQVTPKKRVKRDLAAN 429
-!- SUBCELLULAR LOCATION: Type I membrane protein. Cell wall.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
-!- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 WNGYQ----LVIAMMGIPNQNDNHIYLLYNKYGDNELSHWKNVGPIFGYNSTAVSQEWSGS 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               430 ENNQOKIELTVSPENITVYEGEDVKFTVTAKSDSKTT--LDFSDLLTKYNPSVSDRISTN 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 AVLNSDNSIQLFYTRVDTSDNNTNHQKIASATLYLTDNNGNVSLAQVRNDYIVFEGDGYY 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 SSTSSAASL-----NNT------DSKAAQENTNTAKNDDTQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW; 65DE94AF720A5474 CRC64;
                                                                                                                                                                                                                                                                 Pfam; PF00146; Gram.pos_anchor; 1.
SMART; SM00409; IG; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
Cell wall; Transmembrane; Receptor; Repeat; Signal; Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                        FC RECEPTOR
                                                                                                                                                                                                                     PIR; S15330; PCSOAG,
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                        IGA
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TRANSMEM
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488	QY 395 YQTYDQWKATNKGADNIAMRDAHVIEDGNGDRYLVFEASTGLENYQGEDQI 445	446 YNWLNYGGDDAFNIKSLFRILSNDDIKSRATWANAAIGILKLNKDE	PSNÈ	630 SSKYYTEHYENKYKSDEMYYÖLHAOMEMITRKVVOMMKYDINI ETT ETT ETT ETT ETT ETT ETT ETT ETT ET		i⊣	602 DOVLVTSYMTNRUGVAGKGMDSTWAPSFLLQINPDNTTTVLAKMTNQGDWIMDD 65	740 DQAKEKAKIAVSKYMSKVLDGVHQHLQKKNNSKIVDLFKEL 7	0		840	RESULT 15 SSPS_STRGN ID SSPS_STRGN STANDARD; PRT; 1500 AA. AC P16952; 054184;	01-AUG-1990 (Rel. 15, Created) 15-707-1998 (Rel. 36, Last sequence update)	JOURNIT 2000 (Rel. 39, Last annotatic Agglutinin receptor precursor (SSP-5 SSP5 OR SSPR	Streptococcus gordonii. Bacteria: Firmicutes: Bacillus/Clostridium canada	OC Streptococcus.  OX NCBL_TaxID=1302;		MEDLINE-90236997; Pubmed-2185241 Demuth D.R. Golinh F.F. Malamid	"Streptococal-host interactions. Structural and of a Streptococcus sanguis repentor for a human	glycoprotein."; J. Biol. Chem. 265:7120-7126(1990)	[2] REVISIONS, SEQUENCE FROM N.A.	STWAIN=M5; MEDLINE=96310377; PubMed=8733238; Demuth D P Diam	Jenkinson H.F.;	media humar	MOL. Microbiol. 20:403-413(1996)1- FUNCTION: MAY BIND SIALIC ACID RESI (SAG) IN A CALCIUM-DEPENDENT REACTI ITS RECEPTOR IN VARIOUS ORAL STREPT	OF DENTITY CARIES.	C DOMAIN: THE PR2 REGION. BY SIMILARITY WITH THE PROLINE RICH DOMAINS OF THE S. PYOGENES M6 PROTEIN AND STAPHYLOCOCCAL PROTEIN A, C. MAY TRAVERSE THE CELL WALL PEPTIDOGLYCAN AND IS FOLLOWED BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRO-RICH (PR2).
CONSERVED IN GRAM-POSITIVE COCCI SURFACE PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAASDTTIRTSANANSASSAANTQNSNSQVASSAAITSSTSSAASLNNT-DSKAAQENTN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 SQVAK---ESQAKAGSKESALPVEVSSADLDKAVADAKSAGVKVVQDETKDKGTATTATD 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 TAKNDDTQKAAPANESSEA-----KNEPAVN-----VNDSSAAKNDDQQSSKK---- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----FSKAAKSGTQMTVNDFQKIADTLIKQDGRYTVPFFKASEIKNMPAATTKDAQTNT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 EAKEAYEKAVKENT--AKNEALKVENEAIKQ-------RNETAKATYEAAMKQ 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 YEA----DLAAIKKANEDNDADYQAKLAAYQTELARVQKANAEAKEAYDKAVKENTAKNT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 KSGKNWAVVTLSTAALVFGATTVNASADTNIENNDSSTVQVTTGDNDIAVKSVTLGSGQV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 KVAKTLCGAVLGTALIAFADKAV--FADEVTETTSTSTVEVATTGN--PATNLPEAGGEM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --YGDNELSHWKNVGPIFGYNSTAVSQEWSGSAVLNSDNSIQLFYTRVDTSDNNTNHQKI 362
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                          -!- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
-!- SIMILARITY: BELONGS TO THE SPAP/SSP5/SPAA FAMILY.
                                                                                                                                                                                                                                                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TO M PROTEIN OF S.PYGENES.
4 X APPROXIMATE TANDEM REPEATS, HRI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 EVEKINTANATAKAEYEAKLAQYQKDLATVKKANEDSQQDYQNKLSAYQTELARVQKANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 IEPLDVWDSWPVQDVRTGQVANWN----GYQLVIANMGIPNQNDNHIYLLYNK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                      X APPROXIMATE TANDEM REPEATS, PRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 1500;
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MW; DCF190E7D44D889F CRC64;
                                                                                                                                                                                                                                                                                                 AGGLUTININ RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.6%; Score 229.5; DB 1; Best Local Similarity 20.7%; Pred. No. 0.00041; Matches 196; Conservative 120; Mismatches 368;
                                                                                                                                                                                                                                  Pfam; PF00746; Gram_pos_anchor.
PROSITE: PS00343; GRAM_POS_ANCHORING; 1.
Signal; Repeat; Calcium-binding; Transmembrane.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
POTENTIAL.
POTENTIAL.
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PIR; A35186; A35186.
InterPro; IPR001899; Gram_pos_anchor.
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ASATLYLDNNGNVSLAQVRNDYIVFEGDGYYYQTYDQWKATNKGADNIAMRDAHVIEDG		TINEDRAKSKAYSYFNAINSNNTYGSND		590 KSYYAVPVAGKDDQVLVTSYMTHRNGVAGKGMDSTWAPS-FLLQINPDNTTTVLAKMT 6. :: ::  :	NGGDWIWDDSSENLDMIGDLDSAALPGERDKPUDDLIGY		:
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Search completed: September 26, 2002, 18:26:43 Job time: 182 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

September 26, 2002, 18:23:41; Search time 40.2 Seconds (without alignments) 1885.932 Million cell updates/sec

US-09-995-587A-1 4129 1 MYKSGKNWAVVTLSTAALVF......GMGTLLSMFGLAEINKRRFN 789 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		မ (EC	o)	o)	_	Ξ	Levansucrase - Zym	_	Levansucrase (EC 2	r S	levansucrase - Erw	hypothetical prote	fibronectin-bindin	fibronectin-bindin	IgA Fc receptor pr	Fc receptor	thetical pro			-	dextranase - stren	probable nextideel	protein many 10 fi	process F4NZ.IU [1	Mypornerical prote	Sporozoite surface	rmts protein [impo	Sallva-interacting	Surface antigen pa		Q
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210.5 208.5 208.5	206	202.5 202 199	198.5	196.5 196	195.5 195.5 195
30 31 32	33 34 34	35 37	300	444	4 4 4 6 4 4 0

## ALIGNMENTS

RESULT 1 B28551 B285521 Beansucrase (EC 2.4.1.10) precursor - Streptococcus mutans (strain GS-5) N;Alternate names: sucrose 6-fructosyl transferase C;Species: Streptococcus mutans C;Species: Streptococcus mutans C;Bacte: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 15-Oct-1999 R;Shiroza, T.; Kuramitsu, H.K. J. Bacteriol. 170, 810-816, 1988 A;Title: Sequence analysis of the Streptococcus mutans fructosyltransferase gene an A;Accession: B28551 A;Reference number: A91892; MUD:88115184 A;Reference number: A91892; MUD:88115184 A;Residues: 1-797 < SHI> A;Residues: 1-797 < SHI> A;Residues: 1-797 < SHI> A;Cross-references: GB:M18954; NID:9153635; PIDN:AAA88584.1; PID:9153636 C;Reywords: 91ycosyltransferase; hexosyltransferase	Ouery Match Best Local Similarity 50.4%; Pred. No. 9.1e-97; Matches 408; Conservative 118; Mismatches 211; Indels 73; Gaps 14;	1 MYKSGKNWAVVTLSTAALV-FGATTVNASADTNIENNDSSTVQVTTGDNDIAVKSVTLGS 59 	60 GQVSAASDTTIRTSANANSASSAANTQNSNSQVASSAAITSSTSSAASLNNTDSKAAQ 117 	118 ENTNTAKNDDTQKAAPANESSEAKNEPAVNVNDSSAAKNDDQQSSKKNTTAKLNK 172 	173 DAENVVKRAGIDPNSLTDDOIKALNKMNESKAAKSGTQMTYNDFQKIADTLIKQDGRYTV 232   : :    :     ::    :     :      :       :	233 PFFKASEIKNMPAATTKDAQTNTIEPLDVWDSWPVQDVRTGQVANWNGYQLVIAMMGIPN 292 	293 QNDNHIYLLYNKYGDNELSHWKNVGPIFGYNSTAVSQEWSGSAVLNSDNSIQLFYTRVDT 352 	353 SDNNTNHQKIASATLYLTDNNGNYSLAQVRNDYIVF-EG-DGYYYQTYDQWKATNKGADN 410     : : :: :  :
RESULT B28551 Ilevans N. Alten N. Spate C. Spece C. Accee T. Batr A. Title A. Title A. Accee A. A. Accee A. Molec A. Refet A. Molec A. Resid A. Res	Query Best Match	<b>~</b> 0		П				
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411 IAMRDAHVIEDGNGDRYLVFEASTGLENYQGEDQIYNWLNYGGDDAFNIKSLFRILSNDD 470

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17;

Gaps

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Length 473;

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A) Status: nucleic acid sequence not shown; translation not shown
A) Status: nucleic acid sequence not shown; translation not shown
A) Molecule type: DNA
A) Rolecule type: DNA
A) Rolecule type: DNA
A) Rolecule type: DNA
A) Rolecules: Strain 168
A) Experimental source: strain 168
C) Senetics:
A) Gene: sacs
C) Status protein; glycosyltransferase; hexosyltransferase
E) Rolecules: signal sequence #status predicted <SIG>
E) T-29/Domain: signal sequence #status predicted <MAT>
E) T-30/Product: Levansucrase #status predicted <MAT>
E) T-30/Productis T-40/Productis T
                                                                          E.; Yoshikawa, H.; Danchin, A. of the Gram-positive bacterium Bacillus subtil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QDGRYTVPFFKASEIKNMPAATTKDAQTNTIEPLDVWDSWPVQDVRTGQVANWNGYQLVI 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 AMMGIP-NQNDNHIYLLYNKYGDNELSHWKNVGPI----FGYNSTAV---SQEWSGSA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTYDOW--KATNKGADNIAMRDAHVIEDGNGDRYLVFEASTGLEN-YOGEDQIYNWLNYG 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 KSTSFFRQESQKLLQSDK-KRTAELANGALGMIELNDDYTLKKVMK---PLIASNTVTDE 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNIKKFAKQATVLTFTTALLAGGATQAFAKETNOKPYKETYGISHITRHDMLQIPEQ--Q 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               336 VLNSDNSIQLFYTRVDTSDNNTNHQKIASATLYLTDNNGNVSLAQVRNDYIVFEGDGYYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         453 GDDAFNIKSLFRILSNDDIKSRATWANAAIGILKLNKDEKNPKVAELYSPLISAPMVSDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.0%; Score 744; DB 2; Length 47; 36.8%; Pred. No. 2.6e-31; tive 87; Mismatches 151; Indels
                                                          A;Authors: Yoshikawa, H.F.; Zumstein, E.;
A;Title: The complete genome sequence of t
A;Reference number: A69580; MUID:98044033
A;Accession: H69702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     633 INPDNTTTVLAKMTNQG 649
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Best Local Similarity
Matches 183; Conserv
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NiAlternate names: sucrose 6-fructosyl-transferase
C; Species: Bacillus subtilis
C; Date: 16-Aug-1988 #sequence_revision 20-Peb-1995 #text_change 20-Jun-2000
C; Accession: S07309; A25040; I39967; H69702
R; Stetinmetz, M.; 1e Coq, D.; Aymerich, S.; Gonzy-Treboul, G.; Gay, P.
Mol. Gen. Genet. 200, 220-228, 1985
A; Title: The DNA sequence of the gene for the secreted Bacillus subtilis enzyme levansuc A; Recession: S07309; MUID:85295507
A; Rocession: S07309
A; Molecule type: DNA
A; Recession: STED-
A; Cross-references: EMBL:X02730; NID:940118; PIDN:CAA26513.1; PID:9732568
A; Experimental source: Marburg
B; Shimoftsu, H.; Henner, D.J.
J. Bacteriol. 168, 380-388; 1986
A; Title: Modulation of Bacillus subtilis levansucrase gene expression by sucrose and reg
A; Molecule type: number: A25040; MUID:87008406
A; Molecule type: DNA
A; Recession: A25040
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A; Cross-references: GB:RO1897; ND:g143483; PIDN:AAA22724.1; PID:g143484
A; Cross-references: GB:RO1897; ND:g143483; PIDN:AAA22724.1; PID:g143484
A; Erons. S.; Broulliet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, M.; Galler
Koetter, P.; Koningstein, G.; Krogh, S.; Rumano, M.; Kurite, K.; Laptdus, M.F
A; Authors: Labber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
Akuthors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scrollon,
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scrollon,
Akuthors: V.; Yata, K.; Yata, K.; Yoshida, K.; Yata, K.; Yoshida, K.; Yata, K.; Yoshida, K.; Yata, K.; Yoshida, K.; Yoshida, K.; Yata, K.; Yoshida, K.; Yata, K.; Yoshida, K.; Yata, K.; Yoshida, K.; Yata, K.; Yata, K.; Yoshida, K.; Yata, K.; Yata, K.; Yoshida, K.; Yata, K.; Yata, K.; Yoshida, K.; Yata, K.; Yata, K.; Yoshida, K.; Yata, Y.; Yata, Yata, K.; Yata, Yata
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A; Residues: 1-68 <SH1>
A; Residues: 1-68 <SH1>
A; Residues: 1-68 <SH1>
A; Cross-references: GB:M14202; NID:g143485; PIDN:AAA22725.1; PID:g143486
B; Fouet, A.; Arnaud, M.; Kiler, A.; Rapoport, G
Biochem. Biophys. Res. Commun. 119, 795-800, 1984
A; Title: Characterization of the precusor form of the exocellular levansucrase from Baci
A; Reference number: 139967; MUID:84178454
A; Recession: 139967
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-11, I', 13-62 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                           650
398 IAMRDPHVIEDENGDRYLVFEASTGTENYQGEDQIYNFTNYGGSSAYNVKSLFRFLDDQD 457
                                                                                                                         577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WIWDDSSENLDMIGDLDSAALPGERDKPVDWDLI-GYGLKPHDPA--TPNDPETPTPE- 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        707 ------PNTPETPNTPKTPENPGTPQTPNT------PNTPEIPL 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             698 IISFEVSFDGHLVIKPVKVNNDSAGRIDQSRNSGGSLNVAFNVSAGGNISVKPSQKSINN 757
                                                                                                                                                                                                                       471 IKSRATWANAAIGILKLNKDEKNPKVAELYSPLISAPMVSDEIERPNVYKLGNKYYLFAA
                                                                                                                                                                                                                                                                                                                                                                        SYYAVPVAGKDDQVLVTSYMTNRNGVAGKGMDSTWAPSFLLQINPDNTTTVLAKMTNQGD
                                                                                                                                                                                                                                                                                                                                                                                                               740 TPETPKQPETQTNNRLPQTGNNANKAMIGL 769
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JQ0802 Levansucrase (EC 2.4.1.10) precursor - Bacillus amyloliquefaciens
RNAlternate names: 2,6-beta-D-fructan-6-beta-D-fructosyltransferase; sucrose
C; Species: Bacillus amyloliquefaciens
C; Species: Bacillus amyloliquefaciens
C; Accession: JQ0802; S11739
R; Tang, L.B.; Lenstra, R.; Borchert, T.V.; Nagarajan, V.
Gene 96, 89-39; 1990
A; Title: Isolation and characterization of levansucrase-encoding gene from Bacillus
A; Reference number: JQ0802; MUID:91092506
A; Mcference number: JQ0802; MUID:91092506
A; Residues: 1-472 <-TAN>
A; Residues: 1-472 <-TAN>
A; Experimental source: ATCC 23844
A; Experimental source: ATCC 23844

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LTDDQIKALNKMNFSKAAKSGTQMTYNDFQKIADTLIKQDGRYTVPFFKASEIKNMPAAT 247
                                                             248 TKDAQTNTIEPLDVWDSWPVQDVRTGQVANWNGYQLVIAMMGIP-NQNDNHIYLLYNKYG 306
                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     477 SILQQGQLTIDN 488
                                                                                                                                                                                                                                                                                                                                                                                                                644 KMTNQGDWIWDD 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 125; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
               188
                                                                                                              307
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                                                                                                                      18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     levansucrase [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Species: Old #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: F9718
E:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, J.; Bally, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacter.
A:Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 ENVVKKAGI---DPNSLTDDQIKALNKMNFSKAAKSG---TQMTYNDFOKIADTLIKQDG 228
                                                                                                                                                                                   RYTVPFFKASEIKNMPAATTKDAQINTIEPLDVWDSWPVQDVRTGOVANHNGYQLVIAMM 298
                                                                                                                                                                                                   GIP-NQNDNHIYLLXNKYGDNELSHWKNVGPI-----FGYNSTAV---SQEWSGSAVLN 338
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                  SDNSIQLFYTRVDTSDNNTNHQKIASATLYLTDNNGNVSLAQVRNDYIVFEGDGYYYQTY 398
                                                                                                                                                                                                                                                                                                  399 DQW--KATNKGADNIAMRDAHVIEDGNGDRYLVFEASTGLEN-YQGEDQIYNWLNYGGDD 455
                                                                                                                                                                                                                                                                                                                                                 515
                                                                                                                                                      4 KKIVKQATVLTFTTALLAGGATQAFAKENNQKAYKETYGVSHITRHDMLQIPKQ--QQNE 61
                                                                                                                                                                                                                                                                                                                                                                                                PNVVKLGNKYYLFAATRLNRGSNDDAWMNANYAVGDNVAMVGYVADSLTGSYKPLNDSGV 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                   635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  576 VLTASVPANWRTATYSYYAVPVAGKDDQVLVTSYMTNRNGVAGKGMDSTWAPSFLLQINP
                                                                                                                  49;
                                                                                             Length 472;
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                                                                                                                    Indels
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Best Local Similarity 37.2%; Pred. No. 2.2e-29;
Matches 183; Conservative 88; Mismatches 173; Indels
          A;Gene: sacB
C;Keywords: glycosyltransferase; hexosyltransferase
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-472/Product: levansucrase #status predicted <MAT>
                                                                                 Query Match 18.0%; Score 741.5; DB 2; Best Local Similarity 38.1%; Pred. No. 3.5e-31; Matches 188; Conservative 85; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   636 DNTTTVLAKMTNOG 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : |: | : | | 454 NKTSVVKNSILEQG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
Gene: CAC1772
C; Genetics:
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levansucrase [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: H97118
R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gibson, R.;
J; Barcteriol. 183, 4833, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacteriu
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1428 cKUR>
A;Cross-references: GB:AE001437; PIDN:AAK79739.1; PID:g15024744; GSPDB:GN00168
C;Genetics:
A;Gene: CAC1774
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                          NIAMRDAHVIEDGNGDRYLVFEASTGL-ENYQGEDQIYNWLNYGGDDAFNIKSLFRILSN 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 EP-----LDVWDSWPVQDVRTGQVANWNGYQLVIAMMGIPN--QNDNHIYLLXNKYG 306
DNELSHWKNVGPIFGYNSTAV-----SQEWSGSAVLNSDNSIQLFYTRVD--TSDN
                                                                                                           356 NT--NHQKIASATLYLTDNNGN-VSLAQVRNDYIVFE-GDGYYYQTYDQWKATNK--GAD
                                                                                                                                                                                                                                                    DDIKSRATWANAAIGILKLNKDEKNPKVAELYSPLISAPWVSDEIERPNVVKLGNKYYLF
                                                                                                                                                                                                                                                                                                                                   529 AATRLNRGSNDDAWMNANYAVGDNVAMVGYVADSLTGSYKPLNDSGVVLTASVPANWRTA
                                                                                                                                                                                                                                                                                                                                                                                                                        589 TYSYYAVP-VAGKDDQVLVTSYMTNRNGVAGKGM----DSFWAPSFLLQINPDNTTTVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |: || : :| : :|:
| 3 TRKTY----KMISSLMVILAILFIPFLILRHNTGYTSIWSRQQAQNFKC--TKENTAPNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNELSHWKNVGPIFGYNSTAVSQEWSGSAVLNSDNSIQLFYTRVDTSDN--NTNHQKIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.6%; Score 356.5; DB 2;
27.2%; Pred. No. 2.4e-11;
tive 70; Mismatches 176;
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N.A.ternate names: invertase (EC 3.4.1.2b) - Zymomonas mobilis
(C.Species: Jacana) - Bosor: Botechnol. Biocohem. 59, 289-293, 1995
(A.Title: Cloning and characterization of Zymomonas mobilis genes encoding extracellu
(A.Reference number: JC2519; MUID:95218269
(A.Reference number: JC2519; MUID:95218269
(A.Residues: 1-413 < KYO)
(A.Residues: DNA
(A.Residues: J-413 < KYO)
(A.Residues: J-413 < KYO)
(A.Residues: J-413 < KYO)
(A.Residues: J-1 < KYZ)
(A.Residues: J-1 < KYZ)
(A.Residues: J-1 < KYZ)
(A.Reference number: S50037
(A.Reference number: S50037
(A.Reference number: S50037
(A.Residues: DNA
(A.Residues: DNA
(A.Residues: DNA
(A.Residues: DNA
(A.Residues: L104, 'S', 106-107, 'T', 109-413 < RHE)
(C.Genetics: C.Genetics: 
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N:Alternate names: sucrose 6-fructosyltransferase
C:Species: Zymomonas mobilis
C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 EPLDVWDSWPVQDVRTGQVA--NWNGYQLVIANMGIPNQNDNH----IYLLXNKYGDNEL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311 SHWKNVGPIFGYNSTAVSQEWSGSAVL--NSDNSIQLFYTRVDTSDNNTNHQKIASAT-- 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 545 ANYAVG--DNVAMVGYVADS-LTGSYKPLNDSGVVLTASVPANWRTATYSYYAVPVAGKD 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRYLVFEASTGLENYQGEDQIYNWLNYGGDDAFNIKSLFRILSNDDIKSRATWANAAIGI
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                                                                                                                                                        beta-fructofuranosidase (EC 3.2.1.26) - Zymomonas mobilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.2%; Score 298.5; DB 2; 26.8%; Pred. No. 2.3e-08; ive 79; Mismatches 141;
         383 LVGHRSFVTEVKGYGYIPPQIEWLAEDESSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: sucZE3
C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.2%
Best Local Similarity 26.8%
Matches 108; Conservative
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C;Species: Zymomonas mobilis
C;Species: Zymomonas mobilis
C;Species: Zymomonas mobilis
C;Accession: S33771; MUD:9334, 1993
A;Title: Nucleotide sequence of levansucrase gene (levU) of Zymomonas mobilis ZMI (ATCCIA)
A;Accession: S33771; MUD:93305726
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365 ATLYLTDNNGNVSLAQVRNDYIVFEGDGYYYQTYDQMKATNKGADNIAMRDAHVIEDGNG 424
                                                                                                                                                                                                                                       477 WANAAIGILKLNKDEKNPKVAELYSPLISAPWVSDEIERPNVVKLGNKYYLFAATRLNRG 536
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A; Molecule type: DNA
A; Residues: 1-423 <SON>
A; Cross-references: GB:L08093; NID:95880348; PIDN:AAA27695.1; PID:9295699
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                                                                                                                                                        NDDIKSRAȚWANAAIGILK-LNKDEKNPKVAELYSPLISAPMYSDEIERPNVVKLGNKYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 299; DB 2; L
Pred. No. 2.3e-08;
3; Mismatches 156;
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7.2%; Pred
73; P
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09; Conservative
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A:Molecule type: DNA
A:Residues: 1-415 <GEI>
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Best Local Simi
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                Rivorov K.; Yanase, H.; Tonomura, K.; Kawasaki, H.; Sakai, T.

Blosci. Biotechnol. Biochem. 59, 289-293, 1995
A; Ttle: Cloning and characterization of Zymomonas mobilis genes encoding extracellular A; Reference number: JC2519; MUID:95218269
A; Rocession: JC2519
A; Molecule type: DNA
A; Residues: 1-423 < KYO>
A; Accession: DDBJ:DJ7524; NID:9809529; PIDN:BAA04475.1; PID:9809530
A; Accession: PC2376
A; Accession: PC2376
A; Residues: 1-19 < KY2>
A; Molecule type: protein
A; Residues: 1-19 < KY2>
A; Molecule type: protein
C; Genetics:
A;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         extracellular sucrase - 2ymomonas mobilis
C;Species: Zymomonas mobilis
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Mar-1999
C;Accession: S47527
R;Song, K.B.; Lee, S.K.; Joo, H.K.; Rhee, S.K.
Biochim. Biophys. Acta 1219, 163-166, 1994
A;Title: Nucleocide and derived amino acid sequences of an extracellular sucrase gene (A;Accession: S47527; MUID:94368848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.2%; Score 297; DB 2; Length 423;
26.4%; Pred. No. 2.9e-08;
Live 75; Mismatches 155; Indels 102;
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Best Local Similarity 26.49
Matches 119; Conservative
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A;Molecule type: DNA
A;Residues: 1-413 <SON>
A;Cross-references: EMBL:L08094
C:Accession: JC2519; PC2376
R:Kyono, K.; Yanase, H.; Tor
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September 1993 Influence on virulence of the levansucrase gene 22; levansucrase - Erwinia amylovora C;Species: Erwinia amylovora C;Species: Erwinia amylovora C;Accession: S39195 R;Geier, G; Geider, K.K Submitted to the EMBL Data Library, September 1993 A;Reference number: S39195 A;Reference on the EMBL Data Library, September 1993 A;Reference number: S39195 257 EPLDVWDSWPVQDVRTGQVA--NWNGYQLVIAMMGIPNQNDNH----IYLLYNKYGDNEL 310 SHWKNVGPIFGYNSTAVSQEWSGSAVL--NSDNSIQLFYTRVDTSDNNTNHQKIASAT-- 366 95 -- WYYGGHLLQESANTRTAEWSGGTLMAPGSRNQVETFFTST-LFDKNGVREAVAAVTKG 151 424 248 Gaps 484 249 ARCLSPDRTE--WELGPPLLTARGVNDOMERPHVIFQNGLTYLFTISH------------ 295 ANYAVG--DNVAMVGYVADS-LTGSYKPLNDSGVVLTASVPANWRTATYSYYAVPVAGKD 601 A;Cross-references: EMBL:X75079; NID:g433558; PIDN:CAA52972.1; PID:g433559 -LYLTDNNGNVSLAQVRNDYIVFEGDGYYYQTYDQWKATNKGADNIAMRDAHV-IEDGNG DRYLVFEASTGLENYQGEDQIYNWLNYGGDDAFNIKSLFRILSNDDIKSRATWANAAIGI 485 LKLNKDEKNPKVAELYSPLISAPMVSDEIERPNVVKLGNKYYLFAATRLNRGSNDDAMNN 71; Length Indels : || |:: |: | |:348 NNGLVESFINEIIDPKSGKVRAG--GSLAPTVRVELQGHET 386 602 DQVLVTSYMTN----RNGVAGKGMDSTWAPSFLLQINPDNT 638 147; DB 2; 7.1%; Score 291.5; DB 26.4%; Pred. No. 5.3e-08; 1ve 77; Mismatches 147

Gaps 6.8%; Score 281; DB 2; Length 415; 25.6%; Pred. No. 1.9e-07; iive 73; Mismatches 137; Indels 106;

22;

307 DNELSHW-KNVGP--IFGYNSTA----VSQEWSGSAV-LNSDNSIQLFYTRVDTSDNNT 357 

358 NHQKIASATLYLJDNNGNVSLAQVRNDYIVFEGDGYYYQTYDQ---WKATNKGADNIAMR 414

415 D-AHVIEDGNGDRYLVFEASTGLENYQGEDQIY-----NWLNYGGDDAFNIKSLFR 464 

465 ILSNDDIKSRATWANAAIGILKLNKDEKNPKVAELYSPLISAPMYSDEIERPNVYKLGNK 524 

1   1   1   1   1   1   1   1   1   1	fibronectin-binding protein - Staphylococcus aureus C;Species: Staphylococcus aureus C;Stecession: A3192; R;Signaes, C.; Raucci, G.; Joenson R; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeoe A;Title: Nucleotide sequence of the gene for a fibronectin-binding protein from Stap A;Rocession: A3192; MUID:8909898 A;Residues: 1-108 c.SIG A;Residues: 1-108 c.SIG A;Residues: 1-108 d.SIG A;Cross-references: GB-104151 C;Keywords: fibronectin binding Ouery Match Best Local Similarity 18.4%; Pred. No. 1.5e-05; Matches 195; Conservative 146; Mismatches 322; Indels 398; Gaps 50; C;Keywords: 111:
OY 525 YYLPAATRIANGSNDDAWANANTAVODNYANVOTVADSITGSYRPLANDSGVVLTAS 580  Db 298 YYLPT	DD 137 NESSE

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692 Op δ O à fibronectin-binding protein B - Staphylococcus aureus C;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Species: Signos, Signos, Signos, Signos, Signos, Signos, Signos, Signos, K.; Signos, C.; Mueller, H.P.; Lindberg, M.

RESULT 13

Eur. J. Blochem. 202, 1041-1048, 1991
A;Title: Two different genes encode fibronectin binding proteins in Staphylococcus
A;Reference number: S19702; MUID:92111475
A;Accession: S19702
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-940 - 3.0E>
A;Cross-references: EMBL:X62992; NID:949040; PIDN:CAA44726.1; PID:9581562
C;Keywords: fibronectin binding 44; 55 VTLGSGQ-----VSAASDTTIRTSANANSASSAANTONSNSQVASSAALTSSTSSAASLN 109 Query Match 6.0%; Score 246; DB 2; Length 940; Best Local Similarity 18.6%; Pred. No. 3.8e-05; Matches 185; Conservative 135; Mismatches 334; Indels 340; Gaps 110 NTDSKAAQENTNTAKNDDTQKAAPANESSEAKNEPAVNVND--SSAAKNDDQQSS---- 162 163 ----KKNT--TAKLNKDABNVVKKAGIDPNSLTD-----------------------DQIK 194 138 KPRMKRSTDVTAVAEKEVVEETKATGTDVTNKVEVEEGSEIVGHKQDTNVVNPHNAERVT 197 195 ALNKMNFSKAAKSGTQMTYNDFQKIADTLIKQDGRYTVPFFKASEIKNMPAATTKDAQTN 254 255 TIEPLDVWDSWPVQDVRTGQVANWN-------GYGLVIAMMGIPNQN 294 -------MATGELIGERKVRYTFKEYVQEKKDLTAELSLNLFIDPTTVTQKG 288 295 DNHIYLLYNKYGDNELSHWKNVGPIFGYNSTAVSOEWSGSAVLNSDNSIQLFYTRVDT-- 352 | :| | :| :| | :| | 330 KVDGKFSH-----FAYMKPNNQSLSSVTVTGQVTKGNKPGVNNPTVKVYK--HIGSDDL 381 412 A-----MRDAHVIEDGNGDRYLVFEASTGLE-NYQGEDQIYNML----NYGGDDAFNIK 460 551 -----DNVAMVGYVADSLTGSYKPLNDSGVV------LTASVPANWRTATYSYYA 594 552 THENSKHHADVVEYEEDTINPGGGQVTTESNLVEFDEDSTKGIVTGAVSDHTTIEDTKEYT 611 595 V------PVAGKDDQVLVTSYMTNRNGVAGKGMDSTWAPSFLLQINPDNT 638 612 TESNLIELVDELPEEHGQAQGPIEEITENNHHISHSGLGTENGHGNY--GVIEEIEENSH 669 353 -SDNNTNHOKIASATLYLTDNNGNVSLAQVRNDYIVFEGDGYYYQTYDQWKATNKGADNI 461 SLFRILS--NDDIKSRATWANAAIGILKLNKDEKNPKVAELYSPLI--SAPMVSDEIERP 442 FQTHLEGYYNYYYTSNLTWRN---GVAFYSNNAQGDGKDKIKEPIIEHSTPIELEFKSEP 517 NYVKLGNKYYLFAATRLNRGSNDDAWMNANY------AVG-----AVG-----PVEK-----HELIGTIEESNDSKPIDFEYHTAVEGAEGHAEGTIETEEDSIHVDFEES 639 TIVLAKM-----TNQGDWIWDDSSENLDM-----IGDLDSAALP-----673 --GERDKP-----VDWDLIG--YGLKPH-----244 499 551 g ò g ŏ qq òγ g ô g ŏ g ò g ŏ Q g ŏ ò Q δ g ŏ q ò

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700 700 700 700 700 700 700 700 700 700	OY 734 TPEIPLIPPOYSCHNEGOGILEEDTIPPIVPPTPEPPEPEPEPPEPPEPPEPPEPPP 846  OY 734 TPEIPLIPPOYSCHNEGOGILEEDTIPPIVPPTPPEPPEPPEPPPEPPPPPPPPPPPPPPPPPP	complex	F.199-438/Domain: signal sequence #status predicted <a #status="" 194="" <a="" binding="" cauched="" domain:="" f:189-438="" href="Light-478" lepeat;="" predicted="" protein="" transmembrane="">Light-478/Domain: 194 binding #status predicted <a href="Light-188">Light-188</a> Product: Ight-188</a> Predicted <a href="Light-188">Light-188</a> Producted <a href="Light-188">Light-188</a> Pred: No. 9.3e-05 Pred: No. 9.3e-05 Matches 191; Conservative 130; Mismatches 347; Indels 288; Gaps 40;  QY 10 VVTLSTAALVFGA	L A R R R R L L C L C L C L C L C L C L C L

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A;Title: Characterization of an IgA receptor from group B streptococci: specificity for A;Reference number: A60230, MUID:91055597 A;Accession: A60230 A;Molecule type: protein A;Residues: 'X', 39-48, 'X', 50-52, 'X', 54-56 <lin> C;Superiamily: IgA For receptor C;Superiamily: IgA For receptor C;Reywords: cell wall: immunoglobulin receptor; tandem repeat; transmembrane protein F:137-Domain: signal sequence *status predicted <sig>F:137-Domain: signal sequence *status predicted <iga> F:139-438/Domain: IgA binding *status predicted <iga> F:149-56/Domain: IgA binding *status predicted <iga> F:157-915/Region: proline-rich repeats F:167-915/Region: proline-rich repeats F:167-915/Region: cell wall-spanning *status predicted <ima> F:102-1129/Domain: cell wall-spanning *status predicted <ima></ima></ima></iga></iga></iga></sig></lin>	Ouery Match 5.8%; Score 237.5; DB 2; Length 1134; Best Local Similarity 20.1%; Pred. No. 0.00014; Matches 189; Conservative 129; Mismatches 349; Indels 273; Gabs 39.	TTGDNDIAVKSVTLGS 59 :		QY 179 KKAGIDPNSLTDDQIKALNKMNESKAAKSGTOMTYNDFQKIAD 221  Db 270 KKETSSEENTQKVDEHYANSLQNLAQKSLEELDKATTNEQATQVK NQFLENAQKIKETO 328	222 TLIKODGRYTVPFFKASEIKNMPAATTKDAGTNTIEPLDVWDS 1  :  :  :  :  :  :  :  :  :  :  :  :  :	386	35	KATNKGADN	3EDQIYNWLNYGGDDAFNIKS	OY 462 LFRILSNDDIKSRATWANANIGILKLNKDEKNPKVAELYSPLISAP 507  DD 586 IKELMEQPEIPSNPEYGIQKSIWESQKEPIQEAITSFKKIIGDSSKYYTFFNKVVEN 4.1		562 SLTGSYRPLNDSGVVLTASVPANWRTATYSYYAVPVACKDDQVLVTSYMT
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756KVLDGVHQHLQKKNHSKIVDLFKELEAIKOOTIFFITNNK# 706	672 PGERDKPVDWDLIGYGLKPHDPATPNDPTTDTTDTTDTTTDTTTTTTTTTTTTTTTTTTT	797 EVEIDNLVH-DAFSKMNATVAKFOKGLETNTPETPDTPKIPELPOAPDTP	719 TPENPGTPOTPNTPEIPLTPETPKQPETQINNRLPOT 758	856 SPKAPEAPRVPESPKTPEAPHVPESPKTPEPPKT 895
91	2 PGER	7 EVEI	9 TPEN	SPKA
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Search completed: September 26, 2002, 18:25:06 Job time: 85 sec

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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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## ALIGNMENTS

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder. Novel human diagnostic protein #21642. ABG21651 standard; Protein; 881 AA. Tang YT; 30-MAR-2001; 2001WO-US08631. 31-MAR-2000; 2000US-0540217 23-AUG-2000; 2000US-0649167 18-FEB-2002 (first entry) Drmanac RT, Liu C, (HYSE-) HYSEQ INC.

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving cuantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical disorders involving partners are useful in medical cuantitating a polypeptide in protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in capponshible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic maino acid sequences of the invention.

Consideration, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:| :| :| :| :| :| :| 398 sqktvhtegdmnmnikkivkqatvltfttallaggatqafakenngkayketygvshitr 457
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al Similarity 34.4%; Pred. No. 4.6e-41;
237; Conservative 119; Mismatches 253; Indels
                              Claim 20; SEQ ID No 52010; 103pp; English.
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   biodiversity
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Matches 237;
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327 V---SQEWSGSAVLNSDNSIQLFYTRVDTSDNNTNHQKIASATLYLTDNNGNVSLAQVRN 383
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The invention relates to isolate polynucleotide (1) and the propertied (II) sequences. (I) is useful as hybridisation probes, and propertied (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags (II) is useful in gene therapy techniques (II) is useful for generating antibodies against it, detecting or fountitating a polypeptide in tissue, as molecular weight markers and as imaging of sites expressing (II). (I) are useful in medical disorders involving aberrant protein expression or biological activity. (I) and (II) are useful in medical consorters, forensics, gene mapping, identification of mutations in responsible for genetic disorders or other traits to assess biodiversity amino acid sequences ABG00010-ABG30377 represent novel human consideration, but was obtained in electronic format directly from WIPO at the using interval in electronic format directly from WIPO
DSLTGSYKPLNDSGVVLTASVPANWRTATYSYYAVPVAGKDDQVLVTSYMTNRNGVAGKG 620
                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodiversity
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food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                     621 MDSTWAPSFLLQINPDNTTTVLAKMTNQG 649
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849 -katfapsflmnikgnktsvvknsilegg
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23-AUG-2000; 2000US-0649167
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893 AA;

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64 AASDTIIRTSA----NANSASSAANTQNSNSQVA--SSAAITSSTSSAASLNNTDSKAA 116
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Best Local Similarity 34.1%; Pred. No. 1.1e-40;
Matches 217; Conservative 110; Mismatches 232; Indels
                                                                                         N-PSDB; AAS85832
                                                             Drmanac RT,
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                                                                                                                                                                          214 NDFQKIADTLIKQDGRYTVPFFKASEIKNMPAATTKDAQTNTIEPLDVMDSWPVQDVRTG 273
                          7 NWAVVTLSTAA-LVFGATTVNASAD-----TNIENND-SSTVQVTTGDNDIAVKSVTLGS 59
                                                                                                                                                                                                               274 QVANWNGYOLVIAMMGIP-NONDNHIYLLYNKYGDNELSHWKNYGPI-----FGYNSTA 326
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470 hdmlqipkq--qqnekyqvpqfdqstikniesa------kgldvwdswplqna-dg
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Best Local Similarity 34.4%; Pred. No. 4.7e-41;
Matches 237; Conservative 119; Mismatches 253; Indels
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31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, complypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PER) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The man apply and in recombinant production of (III). The collymucleotides are also used in diagnostics as expressed sequence tags of for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or trot treat disease states involving content of the collyment. (II) and its binding partners are useful in medical activity of sites expressing (II). (I) and its binding partners are useful in medical disorders involving aberrant protein expression or biological activity. Crep polypeptide and polynucleotide sequences have applications in capponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and amino acid sequences. ABG00010-ABG30377 represent novel human
                      -YQGEDQIYNWLNYGGDDAFNIKSLFRILSNDDIKSRATWANAAIGILKLNKDEKNPKVA 497
                                                              ELYSPLISAPMYSDEIERPNVVKLGNKYYLFAATRLNRGSNDDAWMNANYAVGDNVAMVG 557
                                                                               558 YVADSLTGSYKPLNDSGVVLTASVPANWRTATYSYYAVPVAGKDDQVLVTSYMTNRNGVA 617
                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                            618 GKGMDSTWAPSFLLQINPDNTTTVLAKMTNQGDWIW 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 52948; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #22580.
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N-PSDB; AAS86776.
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21;
diagnostic amino acid sequences of the invention.
Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                            88 SNSQVASSAAITSSTSSAAS----LNNTDSKAAQENTNTAKNDDTQKAAPANESSEAKNE 143
                                                                                                                                                            144 PAVNVNDSSAAKNDDQQSSKK-NTTAKLNKDAENVVKKAGI---DPNSLTDDQIKALNKM 199
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                344 kgldvwdswplqna-dgtvaeyngyhvvfalagspkdaddtsiymfyqkvgdnsidswkn 402
                                                                                                                                                                                                                                                                                                                                                   366
                                                                                                                                                                                                                                                                                                                                                        367 LYLTDNNGNVSLAQVRNDYIVFEGDGYYYQTYDQW--KATNKGADNIAMRDAHVIEDGNG 424
                                                                                                                                                                                                                                                                                                                                                                                                                                       DRYLVFEASTGLEN-YQGEDQIYNWLNYGGDDAFNIKSLFRILSNDDIKSRATWANAAIG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484 ILKLNKDEKNPKVAELYSPLISAPMVSDEIERPNVVKLGNKYYLFAATRLNRGSNDDAWM 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 NFSKAAKSG---TQMTVNDFQKIADTLIKQDGRYTVPFFKASEIKNNPAATTKDAQTNTI
                                                                                                                                                                                                                                                                                          EPLDVWDSWPVQDVRTGQVANWNGYQLVIAMMGIP-NQNDNHIYLLYNKYGDNELSHWKN
                                                                                                                                                                                                                                                                                                                                        316 VGPI-----FGYNSTAV---SQEWSGSAVLNSDNSIQLFYTRVDTSDNNTNHQKIASAT
                                                                                                                                                                                                                                                           544 NANYAVGDNVAMVGYVADSLTGSYKPLNDSGVVLTASVPANWRTATYSYYAVPVAGKDDQ
                                                                                                                              60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                       Length 736;
                                                                                                                           219; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  604 VLVTSYMTNRNGVAGKGMDSTWAPSFLLQINPDNTTTVLAKMTNQG 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
18.6%; Score 766; DB 22;
Best Local Similarity 35.2%; Pred. No. 3.5e-39;
Matches 206; Conservative 101; Mismatches 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #5581.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG05590 standard; Protein; 774 AA
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                                                             736 AA;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, collypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The collynucleotides are also used in diagnostics as expressed sequence tags contentially dentifying expressed genes. (I) is useful in gene therapy techniques (I). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as imaging of sites expressing (II). (I) are useful for treating antibodies against it, detecting or food supplement. (II) and its binding partners are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences of the invention.

C diagnostic amino acid sequences of the invention.

C diagnostic amino acid sequences of the invention.

Specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNKDAENVVKKAGI----DPNSLTDDQIKALNKMNFSKAAKSG---TQMTYNDFQKIADTL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 IKQDGRYTVPFFKASEIKNMPAATTKDAQTNTIEPLDVWDSWPVQDVRTGQVANWNGYQL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 VIAMMGIP-NQNDNHIYLLYNKYGDNELSHWKNVGPI-----FGYNSTAV---SQEWSG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 SAVLNSDNSIQLFYTRVDTSDNNTNHQKIASATLYLTDNNGNVSLAQVRNDYIVFEGDGY 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 YYQTYDQW--KATNKGADNIAMRDAHVIEDGNGDRYLVFEASTGLEN-YQGEDQIYNWLN 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451 YGGDDAFNIKSLFRILSNDDIKSRATWANAAIGILKLNKDEKNPKVAELYSPLISAPMVS 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEIERPNYVKLGNKYYLFAATRLNRGSNDDAWMNANYAVGDNYAMVGYVADSLFGSYKPL 570
                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                        Claim 20; SEQ ID No 35949; 103pp; English.
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              31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                 WPI; 2001-639362/73.
                                                                                                  Drmanac RT, Liu C,
                                                                 (HYSE-) HYSEQ INC.
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polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The configuration of configuration of configuration are also used in diagnostics as expressed sequence tags of reference normal activity of (II) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. Consolides in mapping, identification of mutations and to produce other types of data and products dependent on DNA and configuration expression or biological activity. Consolide for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences of the invention.

Configuration, but was obtained in electronic format directly from WIPO xxx
341 deieranvfkmngkwylftdsrgskmtidg--insn----dlymlgyvsnsltgpykpl 393
                                                      571 NDSGVVLTASVPANWRTATYSYYAVPVAGKDDQVLVTSYMTNRNGVAGKGMDSTWAPSFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID No 42113; 103pp; English.
                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #11745.
                                                                                                                                                                                                                       ABG11754 standard; Protein; 774 AA
                                                                                                                                       mnikgnktsvvknsilegggltw 473
                                                                                                     631 LQINPDNTTTVLAKMTNQGDWIW
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23-AUG-2000; 2000US-0649167.
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774 AA;

Sequence

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18;
                                       170 LINKDAENVVKKAGI----DPNSLTDDQIKALNKMNFSKAAKSG----TQMTYNDFQKIADTL 223
                                                                               224 IKQDGRYTVPFFKASEIKNMPAATTKDAQTNTIEPLDVWDSWPVQDVRTGQVANWNGYQL 283
                                                                                            VIAMMGIP-NQNDNHIYLLXNKYGDNELSHWKNVGPI-----FGYNSTAV---SQEWSG 333
                                                                                                                                    SAVLNSDNSIQLFYTRVDTSDNNTNHQKIASATLYLTDNNCNVSLAQVRNDYIVFEGDGY 393
                                                                                                                                                                           394 YYQTYDQW--KATNKGADNIAMRDAHVIEDGNGDRYLVFEASTGLEN-YQGEDQIYNWLN 450
                                                                                                                                                                                                                                             451 YGGDDAFNIKSLFRILSNDDIKSRATWANAAIGILKLNKDEKNPKVAELYSPLISAPMVS 510
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| mmmikkivkqatvltfttallaggatqafakennqkayketygvshitrhdmlqipkq- 59
                                                                                                                                                                                                                                                          285 ygggtnffrkesgk-lggsakkrdaelangalgiielnndytlkvmk---plitsntvt 340
                                 Gaps
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                                                                                                                                                                                                                                                                                                                                          DEIERPNYVKLGNKYYLFAATRLNRGSNDDAWNNANYAVGDNVAMVGYVADSLTGSYKPL
                               49;
        DB 22; Length 774;
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food supplement; medical imaging; diagnostic; genetic disorder.
   18.4%; Score 760.5; DB 22; Length 38.0%; Pred. No. 8.2e-39; tive 87; Mismatches 176; Indels
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23-AUG-2000; 2000US-0649167
                        Conservative
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           Similarity
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                      191;
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Query Match
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Tang YT;

Drmanac RT, Liu C, WPI; 2001-639362/73

N-PSDB; AAS69133

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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, collypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The collynuclectides are also used in diagnostics as expressed sequence tags correspond activity of (II) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or constructivity of (II) or to treat disease states involving considers involving antibodies against it, detecting or a food supplement. (II) and its binding partners are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in the polypeptide and polynuclectide sequences have applications in cresponsible for generic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and to produce other types of data and products dependent on DNA and cid sequence at for this patent did not appear in the printed sequence data for this patent did not appear in the printed set in the form which is the contact of the second sequence data for this patent did not appear in the printed set for this patent did not appear in the printed set for this patent did not appear in the printed set for this patent did not appear in the printed set for this patent did not appear in the printed set for this patent did not appear in the printed set for this patent did not appear in the printed set for the set for this patent did not appear in the printed set for the set for this patent did not appear in the printed set for the set
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 SWPVQDVRTGQVANWNGYQLVIAMMGIP-NQNDNHIYLLYNKYGDNELSHWKNVGPI--- 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                320 ---FGYNSTAV---SQEWSGSAVLNSDNSIQLFYTRVDTSDNNTNHQKIASATLYLTDNN 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASTGLEN-YQGEDQIYNWLNYGGDDAFNIKSLFRILSNDDIKSRATWANAAIGILKLNKD 490
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-diymlgyvsnsltgpykplnktglvlqmgldpndvtftyshfavpqa-kgnnvvitsym 747
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                               Claim 20; SEQ ID No 35305; 103pp; English.
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (C io. identifying expressed genes. (I) is useful in gene therapy techniques (C ii). (II) is useful for generating antibodies against it, detecting or guantitating a polypeptide in tissue, as molecular weight markers and as inogolar protein and its binding partners are useful in medical clisorders involving abereat protein expression or biological activity. (I magnostics, forensics, gene mapping, identification of mutations in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences of the invention.

C diagnostic amino acid sequences of the invention.

C Note: The sequence data for this patent did not appear in the printed cat fire. who, int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.4%; Score 759.5; DB 22; Length 789; 37.2%; Pred. No. 9.7e-39; tive 90; Mismatches 187; Indels 49; Gaps
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                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                Novel human diagnostic protein #28398.
                              ABG28407 standard; Protein; 789 AA
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23-AUG-2000; 2000US-0649167.
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SWPVQDVRTGQVANWNGYQLVIAMMGIP-NQNDNHIYLLYNKYGDNELSHWKNVGPI--- 319
356 etygvshitrhdmlqipkq--qqnekyqvpqfdqstikniesa-----kgldvwd 403
                                       320 ---FGYNSTAV---SQEWSGSAVLNSDNSIQLFYTRVDTSDNNTNHQKIASATLYLTDNN 373
                                                                                       463 sdkfdandpilkdgtqewsgsatftsdgkirlfyt--dysgkhygkqslttaqvnvsksd 520
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                                                                                                                                                                                                                                                                                     chromosome
                                                                                                                        374 GNVSLAQVRNDYIVFEGDGYYYQTYDQW--KATNKGADNIAMRDAHVIEDGNGDRYLVFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #21593.
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23-AUG-2000; 2000US-0649167.
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Cc for identifying expressed genes. (I) is useful in gene therapy techniques of to restore normal activity of (II) or to treat disease states involving cc (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as imaging of suppeptide in tissue, as molecular weight markers and as imaging of suppeptide in tissue, as molecular weight markers and as imaging of sites expressing (II). (I) and its binding partners are useful in medical disorders involving aberrant protein expression or biological activity. (C diagnostics, forensics, gene mapping, identification of mutations in capponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences and products dependent on DNA and diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed capporation; but was obtained in electronic format directly from WIPO vy
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18.4%; Score 759.5; DB 22;
Best Local Similarity 32.3%; Pred. No. 1.5e-38;
Matches 221; Conservative 118; Mismatches 252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID No 52182; 103pp; English.
                                                                                                                                                                                            Novel human diagnostic protein #21814.
                                          ABG21823 standard; Protein; 1095 AA.
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Best Local Similarity 32.3%; Pro
Matches 221; Conservative 118;
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23-AUG-2000; 2000US-0649167.
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ASLNNTDSKAAQENTNTAKNDDTQKAAPANESSEAKNEPAVNVNDSSAAKNDDQQSSKK- 164
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ipkq--qqnekyqvpqfdqstikniesa------kgldvwdswplqna-dgtvaey 723
                                                                                                                                     NGYQLVIAMMGIP-NQNDNHIYLLYNKYGDNELSHWKNVGPI-----FGYNSTAV---S 328
                                                                                                                                                                                                           EGDGYYYQTYDQW--KATNKGADNIAMRDAHVIEDGNGDRYLVFEASTGLEN-YQGEDQI 445
                                                                                                                                               446 YNWLNYGGDDAFNIKSLFRILSNDDIKSRATWANAAIGILKLNKDEKNPKVAELXSPLIS 505
                                                                                                                                                                                                                                                          APMVSDEIERPNVVKLGNKYYLFAATRLNRGSNDDAWMNANYAVGDNVAMVGYVADSLTG 565
                                                                                                                                                                                                                                                                                                                      SYKPLNDSGVVLTASVPANWRTATYSYYAVPVAGKDDQVLVTSYMTNRNGVAGKGMDSTW 625
                                     165 NTTAKLNKDAENVVKKAGI---DPNSLTDDQIKALNKMNFSKAAKSG---TQMTYNDFQK
                                                                                                219 IADTLIKQDGRYTVPFFKASEIKNMPAATTKDAQTNTIEPLDVWDSWPVQDVRTGQVANW
                                                                                                                                                                                   QEWSGSAVLNSDNSIQLFYTRVDTSDNNTNHQKIASATLYLTDNNGNVSLAQVRNDYIVF
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2000US-0649167
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23-AUG-2000;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The analysing expressed generation (FCR) primers, oligomers, and for chromosome operation of (II) and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags to restore normal activity of (II) or to treat disease states involving contribution and its binding partners are useful in medical afood supplement. (II) and its binding partners are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences of the invention.

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18.4%; Score 758.5; DB 22; Length
Best Local Similarity 37.6%; Pred. No. 6.5e-39;
Matches 194; Conservative 90; Mismatches 181; Indels
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                                                                                                                                                             Claim 20; SEQ ID No 34666; 103pp; English.
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359 gvshitrhdmlqipkq--qqnekyqvpqfdqstikniesa------kgldvwdswp 406

209 --TQMTYNDFQKIADTLIKQDGRYTVPFFKASEIKNMPAATTKDAQTNTIEPLDVWDSWP

320 FGYNSTAV---SQEWSGSAVLNSDNSIQLFYTRVDTSDNNTNHQKIASATLYLTDNNGNV 376

VQDVRTGQVANWNGYQLVIAMMGIP-NQNDNHIYLLYNKYGDNELSHWKNVGPI-----

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494 PKVAELYSPLISAPMVSDEIERPNVVKLGNKYYLFAATRLNRGSNDDAWMNANYAVGDNV

554 AMYGYVADSLIGSYKPLNDSGVVLTASVPANWRTATYSYYAVPVAGKDDQVLVTSYMTNR

377 SLAQVRNDYIVFEGDGYYYQTYDQW--KATNKGADNIAMRDAHVIEDGNGDRYLVFEAST

434

641

691

692 ymlgyvsnsitgpykpinktglvlqmgldpndvtftyshfavpqa-kgnnvvitsymtnr 750

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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                   Claim 20; SEQ ID No 53564; 103pp; English.
                                            Novel human diagnostic protein #23196.
     ABG23205 standard; Protein; 789 AA.
                                                                                                                                                                     Tang YT;
                                                                                                                    30-MAR-2001; 2001WO-US08631.
                                                                                                                                 31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                 (first entry)
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N-PSDB; AAS87392.
                                                                                                                                                                    Drmanac RT, Liu C,
                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                  789 AA;
                                                                                           WO200175067-A2.
                                                                              Homo saptens.
                                18-FEB-2002
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                   ABG23205;
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ABG23205
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The and gene mapping a also used in diagnostics as expressed sequence tags (or identifying expressed genes. (I) is useful in gene therapy techniques of the commal activity of (II) or to treat disease states involving (I). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as function of sites expressing (II). (I) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in capponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostics amino acid sequences of the invention.

Companies of the companies of the invention.

Companies of the companies of the printed or specification, but was obtained in electronic format directly from WIPO are format directly from WIPO.
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity |\cdot\>
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

30-MAR-2001; 2001WO-US08631 31-MAR-2000; 2000US-0540217.

WO200175067-A2. Homo sapiens.

11-OCT-2001.

Novel human diagnostic protein #25760.

(first entry)

18-FEB-2002

ABG25769 standard; Protein; 823 AA.

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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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155 KNDDQQSSKK--NTTAKLNKDAENVVKKAGI---DPNSLTDDQIKALNKMNFSKAAKSG- 208
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                                                                                                                                                                                                                                                                                     18.4%; Score 758.5; DB 22; Length 789; 37.6%; Pred. No. 1.1e-38; tive 90; Mismatches 181; Indels 51;
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Best Local Similarity 37.69 Matches 194; Conservative

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Query Match

us-09-995-587a-1.rag

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

30-MAR-2001; 2001WO-US08631. 31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167.

WO200175067-A2. Homo sapiens.

11-OCT-2001.

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polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerisestates are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (I) restore normal activity of (II) is useful in gene therapy techniques (II) (II) is useful for generating antibodies against it, detecting or a food supplement. (II) and its binding partners are useful in medical mading of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. (I per produce other types of data and products dependent on partners are assess biodiversity and or genetic disorders or other traits to assess biodiversity and ocid sequences. Association and products dependent on DNA and diagnostic amino acid sequences of the invention.

Combined and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences of the invention.

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Matches 194; Conserv
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New isolated polynucleotide and encoded polypeptides, useful in dignostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

WPI; 2001-639362/73. Drmanac RT, Liu C, (HYSE-) HYSEQ INC.

N-PSDB; AAS85834

Claim 20; SEQ ID No 52006; 103pp; English.

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, collypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The collynucleotides are also used in diagnostics as expressed agenected for indiagnostics as expressed agenected for its useful in gene therapy techniques (I) constone normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as imaging of sites expressing (II). (I) and its binding pattners are useful in medical disorders involving aberrant protein expression or biological activity. (I) and its binding pattners are useful in medical disorders involving aberrant protein expression or biological activity. (I) and its binding pattners are useful in medical disorders involving aberrant protein expression or biological activity. (I) and its binding pattners are useful in medical disorders or produce other treating and (II). (I) and (II) are useful for treating content treations in responsible for genetic disorders or other traits to assess biodiversity amino acid sequences. Abg000010-ABG30377 represent nowel human or diagnostic amino acid sequences of the invention.

Configuration, but was obtained in electronic format directly from WIPO very
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Novel human diagnostic protein #21638.

18-FEB-2002 (first entry)

ABG21647 standard; Protein; 493

diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

88888888888888

546 AA;

Sequence

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GLEN-YQGEDQIYNWLNYGGDDAFNIKSLFRILSNDDIKSRATWANAAIGILKLNKDEKN 493
                                         554 AMVGYVADSLIGSYKPLNDSGVVLTASVPANWRTATYSYXAVPVAGKDDQVLVTSYMINR 613
                                                                                                     SLAQVRNDYIVFEGDGYYYQTYDQW--KATNKGADNIAMRDAHVIEDGNGDRYLVFEAST
          494 PKVAELYSPLISAPMVSDEIERPNVVKLGNKYYLFAATRLNRGSNDDAWMNANYAVGDNV
                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; dlagnostic; genetic disorder.
                                                                                                                         614 NGVAGKGMDSTWAPSFLLQINPDNTTTVLAKMTNQG 649
                                                                                                                                  455 gffedk--katfapsflmnikgnktsvvknsilegg 488
                                                                                                                                                                                                                            Novel human diagnostic protein #21823.
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                                                                                                                                                                              ABG21832 standard; Protein; 546
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23-AUG-2000; 2000US-0649167.
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N-PSDB; AAS86019.
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                                                                                                    254 NTIEPLDVWDSWPVQDVRTGQVANWNGYQLVIAMMGIP-NQNDNHIYLLXNKYGDNELSH
                                                                                                                                          481 AIGILKLNKDEKNPKVAELYSPLISAPMVSDEIERPNVVKLGNKYYLFAATRLNRGSNDD
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        Length 546;
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                           Indels
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 18.3%; Score 756; DB 22; 36.9%; Pred. No. 9.7e-39; 1ve 95; Mismatches 189;
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

Claim 20; SEQ ID No 52191; 103pp; English.

biodiversity

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerses chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical aforders involving aborates involving disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in

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-1 MYKSGKNWAVVTLSTAALVF......GMGTLLSMFGLAEINKRRFN 789
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US-08-943-374-2
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US-07-638-431-2
PCT-US92-00018-2
5352450-2
US-08-409-995-4
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GenCore version 4.5
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US-08-923-992A-8
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                                                                                                             OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
Sequence:
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28 183.5 4.4 2314 4 US-09-268-347-49 29 183 4.4 1566 2 US-08-666-23 31 182 4.4 1296 3 US-08-66-66-23 32 181.5 4.4 1296 3 US-08-407-260-3 33 181.5 4.4 1296 3 US-08-407-260-3 33 181.5 4.4 1296 3 US-08-407-260-3 34 180.5 4.4 1702 4 US-09-266-347-3 35 180.5 4.4 1702 4 US-08-26-791-2 35 180.5 4.4 1702 4 US-08-26-791-2 36 179.5 4.3 1287 7 US-08-20-202-2 37 179.5 4.3 1287 7 US-08-20-202-2 38 179.5 4.3 1287 7 US-08-20-202-2 39 179.5 4.3 1287 7 US-08-20-202-2 39 179.5 4.3 1287 7 US-08-702-19-2 39 175.5 4.3 1287 5 PCT-US99-02219-2 39 176.5 4.3 1287 5 PCT-US99-1061A-4 30 176.5 4.3 126.5 PCM-USPB-1061A-4 30 176.5 PCM-USPB-1061A-4 30 176.5 PCM-USPB-1061A-4 30 176.5 PCM-USPB-1061A-4 30 17

17;

Indels 53; Gaps

Length 455;

14.7%; Score 606.5; DB 2; 36.2%; Pred. No. 4.2e-36; tive 75; Mismatches 147;

Query Match
Best Local Similarity 36.28
Matches 156; Conservative

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US-08-943-374-2
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APPLICANT: WILMITZER, Lothar
TITLE OF INVENTION: DNA sequences which lead to the
TITLE OF INVENTION: formation of polyfructans (levans), plasmids containing
TITLE OF INVENTION: these sequences as well as a process for preparing
TITLE OF INVENTION: transgenic plants.
                            289 GIP-NQNDNHIYLLYNKYGDNELSHWKNVGPIFGYNSTAV-----SQEWSGSAVLN 338
                                                SDNSIQLFYTRVDTSDN-----NTNHQKIASATLYLTD-NNGNVSLAQVRNDXIVFE-G 390
                                                                                                     391 DGYYYQTYDQWKATNK--GADNIAMRDAHVIEDGNGDRYLVFEASTG-LENYQGEDQIYN 447
                                                                                                                                                                                                                   266 KAYYGGSDVFFONEKNKLLQSPK-KQIASLANGALGIVELADDY----TVKSVMKPLVASN 321
                                                                                                                                                                                                                                                       508 MVSDEIERPNVVKLGNKYYLFAATRLNRGSNDDAWMNANYAVGD-NVAMVGYVADSLTGS 566
                                                                                                                                                                                                 448 WLNYGGDDAFNIKSLFRILSNDDIKSRATWANAAIGILKLNKDEKNPKVAELYSPLISAP 507
                                                                                                                                                                                                                                                                          31 QFKVPQFNASAIKNIDSAKGYDKSGNLID-LDVWDSWPLQNA-DGTAANYHGYHIVSALA 88
                                                                                                                                                           567 YKPLNDSGVYLTASVPANWRTATYSYYAVPVAGKDDQVLVTSYMTNRN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTUMER: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,936
FILING DATE: 09-FEB-1995
CLASSICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen STREET: 1180 Avenue of the Americas STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Meilman, Edward A.
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: P/951-108
TELECOMMUNICATION:
TELEPHONE: (212) 382-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: DE P42270618
FILING DATE: 08-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: EP 93 02110
FILING DATE: 09-AUG-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08381936 Patent No. 5792923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEIER, Gebhardt
GEIDER, Klaus
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APPLICANT: ROBER, Manuela
APPLICANT: GEIER, Gebhard
                                                                                                                                                                                                                                                                                                                                                                                                433 LGVNIKGSDTS 443
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Sequence 2, Application US/08943374

Patent No. 602849

GENERAL INFORMATION:
APPLICANT: ROBER, Manuela
APPLICANT: GEIER, Gebhardt
APPLICANT: GEIER, Klaus
APPLICANT: WILMATIZER, Lothar
TITLE OF INVENTION: formation of polyfructans (levans), plasmids containing
TITLE OF INVENTION: tress sequences as well as a process for preparing
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                         257 EPLDVWDSWPVQDVRTGQVANWNGYQLVIAMMGIPN-----QNDNHIYLL----YNKYG 306
                                                                                                                                                                                                                                                                                                                                                                                                                        99 RARICYWYSRTGKDWIFGGRVWAEGVAPTTREWAGTPILLNDRGDIDLYYTCV----T 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 NHQKIASATLYLTDNNGNVSLAQVRNDYIVFEGDGYYYQTYDQ---WKATNKGADNIAMR 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 D-AHVIEDGNGDRYLVFEASTGLENYQGEDQIY-----NMLNYGGDDAFNIKSLFR 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            525 YYLFAATRLNRGSNDDAMMNANYAVGDNV----AMVGYVADSLTGSYKPLNDSGVVLTAS 580
                                                                                                                                                                                                                                                                                                                                   581 VPANWRTATYSYYAVPVAGKDDQVLVTSYMTNRNGVAGKGMD----STWAPSFLLQINPD 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:: |||:: |||:: |
343 NPSSQPFQTXSHYVMP-----NGLVTSFI---DSVPWKGKDYRIGGTEAPTVKILLKGD 393
                                                                                                                                                                                                                                                                                                                                                                                      307 DNELSHW-KNVGP--IFGYNSTA----VSQEWSGSAV-LNSDNSIQLFYTRVDTSDNNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 PGATIAKVRGKIVTSDQSVSLEGFQQVTSLFSABGTIYQTEEQNAFWN-----FR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 DPSPFIDRNDGKLYMLFEGN--VAGPRGSHEITQAEMGNVPPGYEDVGG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          465 ILSNDDIKSRATWANAAIGILKLNKDEKNPKVAELYSPLISAPMVSDEIERPNVVKLGNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 415;
                                                                                                                                                                                                                                                 25.6%; Pred. No. 1.4e-12,
tive 73; Mismatches 137; Indels
                                                                                                                                                                                                                                    Score 281; DB 1;
Pred. No. 1.4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Ostrolenk, Faber, Gerb & Soffen
1180 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 10036-8403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TELEFAX: (212) 382-0888
TELEX: 236925
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                    6.88;
                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 25.6%
Matches 109; Conservative
                                                                                                                                         % MOLECULE TYPE: protein US-08-381-936-2
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28;

Gaps

us-09-995-587a-1.rai

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131 AAPANESSEAKN--EPAVNVNDSSAAKNDDQQSSKKNTTAKLNKDAENVVKKAGIDPNSL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 TDDQIKALNKMNFSKAAKSGTQMTYNDFQKIADTLIKQDGRYTVPFFKASEIKNMPAATT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 -----KDAQINTIEPLDVWDSWPVQDVRTGQVANWNGYQLVIANMGIPNQ--NDNHIY-- 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --LLYNKYGDNELSHWKN------VGPIFGYNSTAVSQEWSGSAVLNSDNSI 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 ------GAONEFENFRDPFTFEDPAHPGETFWVFEGNSAM---ORETATCNEADLGY 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             453 --GDDAFNIKSLFRILSNDDIK-SRATWANAAIGILKLNKDEKNPKVA--ELYSPLISAP 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  508 MVSDEIERPNVVKLGNKYYLFAATRLNRGSNDDAWMNANYAVG--DNVAMVGYVADSLTG 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 ROGDPYAE-----TVDDVNASGATYQIGNVGLAK----AKNKQLTEWEFLPPILSAN 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         566 SYKPLN-DSGVVLTASVPANW-------RTATYSYYAVPVAGKDDQVLVTSY 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1:11 | 1:1 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 | 1:4 |
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TITLE OF INVENTION: For its Production and DNA Encoding the Enzyme.
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 IGYFŸRPAĠVPAAERPENGGWTYGGLVFKEGVTGQIFEDOSFSHOTOWSGSARVSKNGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 KLFFTDVAFYRNSDGTNIKPYDPRIALSVGKVKANKKGVTLTGFNKVTDLLQADGTYYOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:|: ||| : |:| | : |:| | : |:| | : |:| | : |:| | : |:| | : |:| | : |:| | : |:| | : |:| | : |:| | : |:| | : |:| | : |:| | : |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
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6.8%; Score 279; DB 4; Length 578;
Best Local Similarity 23.4%; Pred. No. 3.3e-12;
Matches 139; Conservative 83; Mismatches 207; Indels 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             610 MTNRNGVAGKGMDSTWAPSFLLQINPDNTTTVLA---KMTNQGDWIWDDSSEN 659
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TITLE OF INVENTION: BETA-FRUCTOFURANOSIDASE GENE
FILE REFERENCE: 10749-0001-0
CURRENT APPLICATION NUMBER: US/09/503,172A
PRIOR APPLICATION NUMBER: JP 160416/1999
PRIOR APPLICATION NUMBER: JP 160416/1999
PRIOR FILING DATE: 1999-06-08
NUMBER OF SED ID NOS: 9
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08362232
Patent No. 5641667
GENERAL INFORMATION:
APPLICANT:
                                                         TONOZUKA, Takashi
                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Arthrobacter sp.
US-09-503-172A-2
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
LENGTH: 578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 DNELSHW-KNVGP--IFGYNSTA-----VSQEWSGSAV-LNSDNSIQLFYTRVDTSDNNT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 RARICYWYSRTGKDWIFGGRUWAEGVAPTTREWAGTPILLNDRGDIDLYYTCV----T 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NHQKIASATLYLTDNNGNVSLAQVRNDYIVFEGDGYYYQTYDQ---WKATNKGADNIAMR 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 PGATIAKVRGKIVTSDQSVSLEGFQQVTSLFSADGTIYQTEEQNAFWN-----FR 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 : | : | | : : | | | : : | | : | 203 DPSPRIDRNDGKLYMLFEGN--VAGPRGSHEITQAEMGNVPFGYEDVGG------ 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 D-AHVIEDGNGDRYLVFEASTGLENYGGEDQIY-----NMLNYGGDDAFNIKSLFR 464
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40 EEVFINDTMPLRDF-DGEIISVNGWCIIFTLTADRNTDNPQFQDENGNYDITRDWEDRHG 98
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6.8%; Score 281; DB 3; Length 415;
Best Local Similarity 25.6%; Pred. No. 1.4e-12;
Matches 109; Conservative 73; Mismatches 137; Indels 1
PatentIn Release #1.0, Version #1.25
                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/381,936
FILING DATE:
PRIOR APPLICATION NUMBER: DE P42270618
FILING DATE:
PRIOR APPLICATION NUMBER: DE P42270618
FILING DATE: 08-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mellman, Edward A.
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: P/951-108
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 382-0700
TELEFAX: (212) 382-0888
INFORMATION FOR SEQ. ID NO: 2:
                                                                     APPLICATION NUMBER: US/08/943,374
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Sequence 2, Application US/09503172A

Selent No. 6204510

SEREAL INFORMATION:

APPLICANT: ITO, Tetsuya

APPLICANT: FUJITA, KOki

APPLICANT: HARA, KOZO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
TOPOLOGY: linear
                            CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-943-374-2
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350 Jericho Turnpike

Jericho

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Fructosyltransferase Enzyme, Method
For its Production and DNA Encoding the Enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259 -LDVWDSWPVQDVRTGQVANWNGYQLVIAMMGIPNQ----NDNHIY----LLYNKYGDNE 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 -DTSDNN-TNHQKIASATLYLTDNNGNVSLAQVRNDY--IVFEG------DGYYYQ 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 RDANANNITPPDAIITOT------LGRIHADFNHVWFTGFTAHTPLLOPDGVLYO 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397 TYDQWKATNKGADN--IAMRDAHVIEDGN--GDRYLVFEAST----GLENYQGEDQIYNW 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 TOGAYDPOSDFTARWTRADALQIKAHSDATV----AAGGNSLFAQLTMPNIPADFPVINP 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 -----NGAQNEFFNFRDPFTFEDPKHPGVNYMVFFGNTAGQRGVANCTEAD----- 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 LSH----WKNVGPIFGYNSTAV-----SQEWSGSAVLNS--DNSIQLFYTRV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.4%; Score 266; DB 1; Length 543;
26.9%; Pred. No. 2.6e-11;
Live 63; Mismatches 171; Indels 150;
                                                                                                                                                                                                                                                                                      STATE: COUNTRY: United States COUNTRY: United States COUNTRY: 11758
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 Mb COMPUTER: IBM PC compatible OPPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Wordperfect 6.0 for DOS CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/814,196
FILING DATE: 10-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 10-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/362,232
FILING DATE: 22-December-1994
APPLICATION NUMBER: CU 125/93
FILING DATE: 23-December-1993
ATTORNEY/AGENT INFORMATION:
NAME: BAION, RORALD J.
                                                          Sequence 2, Application US/08814196
Patent No. 5731173
GENERAL INFORMATION:
                                                                                                                                                                                                                            ADDRESSEE: Hoffmann & Baron
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Baron, Ronald J.
REGISTRATION NUMBER: 29,281
REFERENCE/POCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (516) 822-3550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.4%
Best Local Similarity 26.9%
Matches 141; Conservative
                                                                                                                                            TITLE OF INVENTION: Fr
TITLE OF INVENTION: FC
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO US-08-814-196-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                  US-08-814-196-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 -LDVWDSWPVQDVRTGQVANWNGYQLVIAMMGIPNQ----NDNHIY----LLXNKYGDNE 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 LSH-----WKNVGPIFGYNSTAV-----SOEWSGSAVLNS--DNSIQLFYTRV--- 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 TQMTY---NDFQ----KIADTL-IKQDGRYTVPFFKASEIKNMPAATTK---DAQTNTIEP 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 DVWVWDTWTLIDKHADOF-SYNGWEVIFCLTADPNAGYGFDDRHVHARIGFFYRRAGIPA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 -DTSDNN-TNHOKIASATLYLTDNNGNVSLAQVRNDY--IVFEG-------DGYYYO 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 SRRPVNGGWTYGGHLFPDGASAQVYAGGTYTNQAEWSGSSRLMQIHGNTVSVFYTDVAFN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 TYDQWKATNKGADN--IAMRDAHVIEDGN--GDRYLVFEAST----GLENYQGEDQIYNW 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   449 LNYGGDDAFNIKSLFRILSNDDIKSRATWANAAIGILKLNKDEKNPKVAELYSPLISAPM 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 TOQAYDPQSDFTARWTRADALQIKAHSDATV----AAGQNSLPAQLTMPNIPADFPVINP 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSDEIERPNVVKLGNKYYLFAATRLNRGSNDDAWMNANYAVG----DNVAMVGYVADSLT 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               565 GSYKPLNDSGVVLTASVPANMRTA------TYSYYAVPVAGKDDQVLVT 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171; Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
6.4%; Score 266; DB 1; Length 543;
Best Local Similarity 26.9%; Pred. No. 2.6e-11;
Matches 141; Conservative 63; Mismatches 171; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SY---MTNRNGVAGKGMDSTWAPSFLLQINPDNTTTVLAKMTNQG 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDUM TYPE: Floppy disk, 3.5 inch, 1.44 Mb COMPUTER: Floppy disk, 3.5 inch, 1.44 Mb COMPUTER: TBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Wordperfect 6.0 for DOS CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/362,232 FILING DATE: 22-December-1994 APPLICATION DATA: APPLICATION NUMBER: CU 125/93 ATTORNEY AGENT INCRMATION: NAME: DATE: 23-December-1993 ATTORNEY AGENT INCRMATION:
New York
                                                                                                                                                                                                                                                                                                 NAME: Baron, Ronald J. REGISTRATION NUMBER: 29,281
REFERENCE/DOCKET NUMBER: 294-29
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3550
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: NO US-08-362-232-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                 COUNTRY:
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LNYGGDDAFNIKSLFRILSNDDIKSRATWANAAIGILKLNKDEKNPKVAELYSPLISAPM 508
                     303 LGERPUDP-NAETLQEVLD----SGAYYQKANIG-LAIATDSTLSK-WKFLSPLISANC 354
                                                      509 VSDEIERPNVVKLGNKYYLFAATRLNRGSNDDAWMNANYAVG----DNVAMVGYVADSLT 564
                                                                                 355 VNDQTERPQVYLHNGKYXIFTISH------RTTFAAGVDGPDGV--YGFVGDGIR 401
                                                                                                                              607
                                                                                                                                 402 SDFQPMN-YGSGLTMGNPTDLNTAAGTDFDPSPDQNPRAFQSYSHYVMPGG-----LVE 454
                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA FC Binding Forms of the Group B
TITLE OF INVENTION: Streptococcal Beta Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 341; Indels 287; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         565 GSYKPLNDSGVVLTASVPANWRTA-------TYSYXAVPVAGKDDQVLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 VVTLSTAALVEGA------VQV 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 TTGDNDIAVKSVTLGSGQVSAASDTTIRTSA----NANSASSAANTQNSNSQVASSAAIT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1164;
                                                                                                                                                                   608 SY---MINRNGVAGKGMDSTWAPSFLLQINPDNTTTVLAKMINQG 649
                                                                                                                                                                                       ADDRESSEE: Sterne, Ressler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
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20.2%; Pred. No. 5.64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA.

PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 60/024,707

FILING DATE: 06-SEP-1996

ATTORNEY AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REGISTRATION NUMBER: 11438.01400f

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA.
APPLICATION DATA.
FILIND DATE: 05-529-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                   Sequence 10, Application US/08923992A
Patent No. 6280738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 193; Conservative 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-923-992A-10
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US-08-923-992A-10
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PTTDIKKAVEPLEKTAGETS-ATDTGKREKOLQOWKNNLKNDVHNTILSHEQKNEFKTKI 139
                                                    SSTSSAASL----NNT-----DSKAAQENTNTAKNDDTQKAAPANESS 138
                                                                                              140 DETNDSDALLELENQFNETNRLLHIKQHEEVEKDKKAKQQ--KTLKQSDT-KVDLSNIDK 196
                                                                                                                                                                                                  197 ELNHOKSQVETMAEQLGITNEDKDSMLKKIEDIRKQAQQADKKEDAEVKVREELGKLFTS 256
                                                                                                                                                                                                                                                          TTAKLNKDAENVVKK-----AGID---PNSLTDDQIKALNKMNFSKAAKSGTQMTYN 214
                                                                                                                                                                                                                                                                                                         257 TKAGLDQEIQEHVKKETTSEENTQKVDEHYPNSLQNLAOKSLEELDKATTNEQATQVK-N 315
                                                                                                                                                                                                                                                                                                                                                              215 DF----QKIAD--TLIKQDGRYTVPFFKA------SEIKNMPAATTKDAQTNTIEPL 259
                                                                                                                                                                                                                                                                                                                                                                                                  316 OFLENAQKIKEIQPLIKET---NVKLYKAMSESLEQVEKQLKHNSQANLEDLVAKSKEIV 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...----WPVQDVRTGQVANWNG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 YQLVIAMMGIPN----QNDNHIYLLYNKYGDNELSHWKNVGPIFGYNSTAVSQEWSGSAV 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           433 QOKIELTVSPENITVYEGEDLKFTLTAKSDSKTTLDFSDL--LTKYN-PSVSDRISTNYK 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 TYDOWKATNKGADNIAMRDAHVIE------DGNGDRYLVFEASTGLENYQGEDQIYN 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         448 WLNYGGDDAFNIKSLFRILSNDDIKS------RATWAN-----AAIGILKLNKDEKN 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           584 ------KAIKELMEQPEIPSNPEYGIQKSIWESQKEPIQEAITSFKKIIGDSSS 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 548 AVGDNVAMVGYVADSLTGSYKPL----NDSGVVLTASVPANWRTATYSYXAVPVAGKDDQ 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----VLVTSYMTNRNGVAGKGMDSTWAPSFLLQINPDNTTTVLAKMTNQGDWIMDDSS 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          742 AKEKAKIAVSKYMS------KVLDGVHQ-----HLQKKNNTKIV-------DLFKELEA 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 783 IKOOTIFDIDNAKTEVEIDNLVH-DAFSKMNATVAKFOKGLETNTPETPHTPKIPELPOA 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            658 ENLDMIGDLDSAALPGERDKPVDWDLIG-----YGLK---PHDPATPNDPETPTT 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08923992A
Sequence 6, Application US/08923992A
GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: Streptococcal Beta Antigens
TITLE OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                337 LNSDNSIOLFYTRVDTSDNNTNHQKIASATLYLTDNNGNVSLAQVRNDYIVFEGDGYYYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 REYEGKLNOSKNLPELKOLEEEAHSKLKOVVEDFRKKFKTSEQVTPKKRVKRDLAANENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       632 KYYTEHYENKYKSDFMNYOLHAQMEMLTRKVVQYINKYPDNAEIKKIFESDMKRTKEDNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   692 GSLENDALKGYFEKYFLTPFNKIKQIVDDLDKKVEQDQPA-----PIPENSEMDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 534 ----OKKEEKQVPKTPEQKDSKTEEKVPQEPKSNDKNQLQELIKSAQQQLEKLE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             494 PKVAELYSPLISAPMVSDEIERP-----NVVKLGNKYYLFAATRLNRGSNDDAMMNANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   705 PETPETPNTPKTPKTPENPGTPQTPNTPNTPEIPLTPETPKQPETQTNNKLPQTGN 760
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DAFNIKSLFRILSNDDIKS-----RATWAN-----AAIGILKLNKDEKNPKVAELY 500
                                                                                                                                                                        603 FNKYKSDFMNYQLHAQMEMLTRKVVQYMNKYPDNAEIKKIFESDMRRTKEDNYGSLENDA 662
                                                                                                                                                                                                                                                                                           605 LVTSYMTNRNGVAGKGMDSTWAPSFLLQINPDNTTTVLAKMTNOGDWIMDDSSENLDMIG 664
                                                                                                                                                                                                                                                                                                                    754 DIDNAKTEVEIDNLVH-DAFSKMNATVAKFOKGLETNTPETPDTPKIPELPQAPDTPGAP 812
                                                                                                                                                                                                                                                                                                                                                                DLDSAALPGERDKPVDWDLIG-----YGLK---PHDPATPNDPETPTTPETPETP 711
                                                                                                           ----KAIKELMEOPEIPSNPEYGIOKSIWESOKEPIOEAITSFKKIIGDSSSKYYTEHY
                                                                                                                                                 501 SPLISAPMYSDEIERP-----NVVKLGNKYYLFAATRLNRGSNDDAMMNANYAVGDNVA
                                                                                                                                                                                                                    555 MVGYVADSLTGSYKPL----NDSGVVLTASVPANWRTATYSYYAVPVAGKDDQ-----V
                                                                                                                                                                                                                                                      663 LKGYPEKYFLTPFNKIKQIVDDLDKKVEQDQPA------PIPENSEMDQAKEKAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 238; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08242932
Patent No. 5595740
GENERAL INFORMATION:
APPLICANT: Brady, L. Jeannine
TITLE OF INVENTION: Cloning of No. 5595740-19A Fc Binding Forms of TITLE OF INVENTION: the Group B Streptococcal Beta Antigens
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
5.9%; Score 242; DB 1; Length 984;
Best Local Similarity 20.7%; Pred. No. 3.5e-09;
Matches 176; Conservative 112; Mismatches 325; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                   712 NTPKTPKTPENPGTPQTPNTPNTPEIPLTPETPKQPETQTNNRLPQT 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                         502 EKQVPKTPEQKDSKTEEKVPQEPKSNDKNQLQELIKSAQQELEKLE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,932
FILING DATE: 16-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION UNDBER: 31,794
REFERENCE/DOCKET NUMBER: UF14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            984 amino acids
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MOLECULE TYPE: protein
US-08-242-932-2
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 NNT-----KAAPANESSEAK- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 --NEPAVNVNDSSAAKNDD-----QQSSKKNTTAKLNKDAENVVK-------KAGID 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 KNWAVVTLSTAALVEGATTVNASADTNIENNDSST-----VQVTTGDNDIAVKSVTLGS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 ---- 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 QEIHEHVKKETSSEENTQKVDEHYANSLQNLAQKSLEELDKATTNEQATQVK-NQFLENA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 OKIAD--TLIKQDGRYTVPFFKA-----SEIKNMPAATTKDAQTNTIEPLDVWDS- 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265 -----WPVQDVRTGQVANWNGYQ---L 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           343 LNQSKNLPELKQLEEEBAHSKLKQVVEDFRKKFKTSEQVTPKKRVKRDLAANENNQOKIEL 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 VIAMMGIPNQNDNHIYLLXNKYGDNELSHWKNVGPIFGYNSTAVSQEWSGSAVLNSDNSI 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403 TVSPENITVYEGEDVKFTVTAKSDSKTT--LDFSDLLTKYNPSVSDRISTNYKTNTDN-- 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 QLFYTRVDTSDNNTNHQKIASATLYLTDNNGNVSLAQVRNDYIVFEGDGYYYQTYDQWKA 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     459 ---HKIAEITIKNLKLNESQTVTLKAKDDSGNV----VEKTFTITV------OKKE 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         404 TNKGADNIAMRDAHVIE-------DGNGDRYLVFEASTGLENYQCEDQIYNWLNYGGD 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.0%; Score 246.5; DB 4; Length 1128;
Conservative 126; Mismatches 343; Indels 287;
                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,992A
FILING DATE: 05-SEP-1997
                                                                                                                                                                                                                                                                                                                                           1438.0140001/RWE
                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-5EP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.014000
                                                                                                                                                                                                                                                                                                                                                            IELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 1128 amino acids
                                                                                        Floppy disk
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 191; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
STATE: D.C.
                              COUNTRY: U
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6 KNWAVVTLSTAALVFGATTVNASADTNIENNDSST-----VQVTTGDNDIAVKSVTLGS 59

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Db 5 KDDSVKTTEVAAKPYPSMAQTDOGNNSSSELETTKMEIPTTDIKKAVEPVEKTA 59  Qy 60 GQVSAASDTTIRTSANANSASSAANTONSNSOVASSAAITSSTSSAASL	4 4 6 6 6 6 6 7 7	NESULT 10  10-08-714-481-2  Sequence 2, Application US/08714481  Patent No. 576606  GENERAL INFORMATION:  FAPLICANT: Brady, L. Jeannine  TITLE OF INVENTION:  TITLE OF INVENTION: the Group B Streptococcal Beta Antigens  CORRESPONDENCE ADDRESS:  ADDRESSEE: Sallwanchik & Saliwanchik  STREET: 2421 N.W. 41st Street, Suite A-1  CITY: Gainesville
		&D

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Query Match
Best Local Similarity 20.7%; Pred. No. 3.5e-09;
Matches 176; Conservative 112; Mismatches 325; Indels 238; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 GOVSAASDTIIRTSA----NANSASSAANTONSNSOVASSAAITSSTSSAASL----- 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 NETNRLLHIKQHEEVEKDKKAKQQ--KTLKQSDT-KVDLSNIDKE-----LNHQKSQVE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 KNDDQQSSKKNTTAKLNKDAENVVKKAGIDPNSLTDDQIKALNKMNFSKAAKSGTQMTYN 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                             COMPUTER REACTION

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: PEDLICATION DARA:
APPLICATION NUMBER: US/08/714,481
FILING DATE: 16-SEP-1996
CLASSIFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/22,932
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAMME: SAILWANCHIN: DAVIG R.
REGISTRATION NUMBER: 31,794
ATTORNEY/AGENT INFORMATION:
NAMME: SAILWANCHIN: DAVIG R.
REFERENCE/DOCKET NUMBER: UF142
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBHONE: 904-375-8100
TELEBHAX: 904-375-5800
INFORMATION FOR SEQ ID NO: 2:
CPONTENCY CHARACTERISTICS:
                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 984 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-714-481-2
32606
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435 IQEAITSFKKIIGDSSSKYYTEHYFNKYKSDFMNYQLHAQMEMLTRKVVQYMNKYPDNAE 494
                                   531 TRLNRGSNDDAMMNANYAVGDNVAMYGYVADSLTGSYKPL----NDSGVVLTASVPANWR 586
                                                                    IKKIFESDMKRTKEDNYGSLENDALKGYFEKYFLTPFNKIKQIVDDLDKKVEQDQPA--- 551
                                                                                                                              640
                                                                                                                                         552 ------PIPENSEMDQAKEKAKIAVSKYMS------KVLDGVHQ-----HLQKKNNSK 592
                                                                                                                                                                                                                                 644
                                                                                                                                                                         641 VLAKMINQGDWIWDDSSENLDMIGDLDSAALPGERDKPVDWDLIG------YGLK- 689
                                                                                                                                                                                                                                              690 --PHDPATPNDPETPTTPETPETPNTPKTPENPGTPOTPNTPNTPETPLTPETPKOP 747
                                                                                                                                                                                                                                                                    587 TATYSYYAVPVAGKDDQ-----VLVTSYMTNRNGVAGKGMDSTWAPSFLLQINPDNTTT
                                                                                                                                                                                                   593 IV------DLFKELEAIKQOTIFDIDNAKTEVEIDNLVH-DAFSKMNATVAKFOKGLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION: Cloning of Non-IgA Fc Binding Forms of
TITLE OF INVENTION: the Group B Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street. Suite A.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 Grinter Hall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: Saliwanchik & Saliwanchik
: 2421 N.W. 41st Street, Suite A-1
Galnesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Postal code/Zip: 32611
Phone number: 904-392-8929
Fax number: 904-392-6600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/242,932
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application PC/TUS9506111 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF142
TELECOMUNICATION INFORMATION:
TELEPHONE: '904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   City: Gainesville
State/Province:
Country: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Street address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Telex number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        984 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
PCT-US95-06111-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                   60 GETS-ATDIGKREKQLQQWKNNLKNDVDNTILSHEQKNEFKTKIDETNDSDALLELENQF 118
                                                                                                                                                                                   109 NNT-------DSKAAQENTNTAKNDDTQKAAPANESSBAKNBPAVNVNDSSAA 154
                                                                                                                                                                                                           119 NETNRLLHIKQHEEVEKDKKAKQQ--KTLKQSDT-KVDLSNIDKE-----LNHQKSQVE 169
                                                                                                                                                                                                                                                155 KNDDQQSSKKNTTAKLNKDAENVVKKAGIDPNSLTDDQIKALNKMNFSKAAKSGTOMTYN 214
                                                                                                                                                                                                                                                                        170 KMAEQKGITNEDKDSMLKKIEDIRKQA-----QQADKKEDAEVKVQLEEERAHSKLKQVVE 224
                                                                                                                                                                                                                                                                                                             215 DFQKIADTLIKQDGRYTVPFFKASE-----IKNMPAATTKDAQ----TNTIEPLDVWD 263
                                                                                                                                                                                                                                                                                                                                           264 SWPVQDVRTGQVANWNGYQLVIAMMGIPNQNDNHIYL----LYNKYGDNELSHWKNVGPI 319
                                                         6 KNWAVYTLSTAALVFGATTVNASADTNIENNDSST-----VQVTTGDNDIAVKSVTLGS 59
                                                                                 320 FGYNSTAVSQEWSGSAVLNSDNSIQLFYTRVDTSDNNTNHQKIASATLYLTDNNGNVSLA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 OVRNDYIVFEGDGYYYQTYDOWKATNKGADNIAMRDAHVIE------DGNGDRYLVF 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              531 TRLNRCSNDDAWMNANYAVGDNVAMVGYVADSLTGSYKPL----NDSGVVLTASVPANWR 586
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                                        Indels 238;
           Length 984;
                                        325;
      DB 5;
             Best Local Similarity 20.7%; Pred. No. 3.5e-09
Matches 176; Conservative 112; Mismatches 32;
      Score 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08923992A
Patent No. 6280738
GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
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705 EAPRVPESPKT 715
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US-08-923-992A-2
Query Match
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335 AVLNSDNSIQLEYTRVDTSDNNTNHQKIASATLYLTDNNGNVSLAQVRNDXIVFEGDGYY 394
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                                                                                                                                                                                               446 YNWLNYGGDDAFNIKSLFRILSNDDIKS-----RATWAN-----AAIGILKLNKDE 491
                                                                                                                                                                                                                           492 KNPKVAELYSPLISAPNVSDEIERP-----NVVKLGNKYYLFAATRLNRGSNDDAWMNA 545
                                                                                                                                                                                                                                                                                                      630 SSKYYTEHYENKYKSDFMNYOLHAQMEMLTRKVVQYMNKYPDNAEIKKIFESDMKRTKED 689
                                                                                                                                                                                                                                                                                                                                                                               690 NYGSLENDALKGYFEKYFLTPFNKIKQIVDDLDKKVEQDQPA------PIPENSEM 739
                                                                                                                                                                                                                                                                                                                                               546 NYAVGDNVAMVGYVADSLTGSYKPL----NDSGVVLTASVPANWRTATYSYYAVPVAGKD 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                  740 DQAKEKAKIAVSKYMS------KVLDGVHQ-----HLQKKNNSKIV-----DLFKEL 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            656 SSENLDMIGDLDSAALPGERDKPVDWDLIG-----YGLK---PHDPATPNDPETP 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08923992A

Patent No. 6280738

GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: Streptococcal Beta Antigens
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                        395 YQTYDQWKATNKGADNIAMRDAHVIE------DGNGDRYLVFEASTGLENYQGEDQI
                                                                                                                                                                                                                                                                                                                                                                                                                     602 DO-----VLVTSYMTNRNGVAGKGMDSTWAPSFLLQINPDNTTTVLAKMTNQGDWIWDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           781 EAIKOGTIFDIDNAKTEVEIDNLVH-DAFSKMNATVAKFOKGLETNTPETPDTPKIPELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         703 TTPETPETPRTPKTPKTPRTPGTPQTPNTPRTPETPLTPETPKQPETQTNNRLPQT 758
                                                                                  488 YKTNIDN-----HKIAEITIKNLKLNESQTVTLKAKDDSGNV----VEKTFTITV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADARRSSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,992A CLASSERVERS 05-SEP-1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1438.0140001/RWE
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER RENDABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 14:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T.C. CADA STATE TO THE SECTION OF THE SECTION OF THE SECTION OF SEC
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TITLE OF INVENTION: No. 6280738-IgA Fc Binding Forms of the Group B TITLE OF INVENTION: Streptococcal Beta Antigens
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.8%; Score 241; DB 4; Length 1164;
Best Local Similarity 20.0%; Pred. No. 5.3e-09;
Matches 191; Conservative 130; Mismatches 347; Indels 288; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSTSSAASL----NNT----- NNT---- DSKAAQENTNTAKNDDTQ----- 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 DETNDSDALLELENGFNETNRLLHIKQHEEVEKDKKAKQO--KTLKQSDTKVDLSNIDKE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 ---KAAPANESSEAK---NEPAVNVNDSSAAKNDD----QOSSKK----- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 LNHQKSQVEKMAEQKGITNED----KDSMLKKIEDIRKQAQQADKKEDAEVKVREELGKL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 K-NQFLENAQKLKEIQPLIKET---NVKLYKAMSESLEQVEKELKHNSEANLEDLVAKSK 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 VVTLSTÄALVEGA-----VQV 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 --NTTAKLNKDAENVVKK-----AGID---PNSLTDDQIKALNKMNFSKAAKSGTQM 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 TYNDF----QKIAD--TLIKQDGRYTVPFFKA-----SEIKNMPAATTKDAQTNTI 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 VASVAVASLEMGSVAHASELVKDDSVKTTEVAAKPYPSMAQTDQGNNSSSSELETTKMEI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 TTGDNDIAVKSVTLGSGQVSAASDTTIRTSA----NANSASSAANTQNSNSQVASSAAIT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIVREYEGKLNQSKNLPELKQLEEEAHSKLKQVVEDFRKKFKTSEQVTPKKRVKRDLAAN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 WNGYQ----LVIAMMGIPNQNDNHIYLLYNKYGDNELSHWKNVGPIFGYNSTAVSOEWSGS 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          430 ENNQQKIELTVSPENITVYEGEDVKFTVTAKSDSKTT--LDFSDLLTKINPSVSDRISTN 487
                                                     AUDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600 STATE: D.C.
                                                                                                                                                                                                                                                     SOFTWARE: Patentin Frous, mo. Lossing #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,992A
FILING DATE: 05-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INCORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 1164 amino acids
amino acid
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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; MOLECULE TYPE: protein
US-08-923-992A-2
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D.C.
USA
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------DTTIRTSANANSASSAANTQNSNSQVASSAAITS 100
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| ETNRLLHIKQHEEVEKDKRAKQQKTLKQSDTKVDLSNIDKELNHQKSQEAGITNEDKDSM 185
                                                                                                                                                                                                                                                                                                 145 AVNVNDSSAAKNDDQQSSKK------180
                                                                                                                                                                                                                                            101 STSSAASLN----NTDSKAAQENT-----NTAKNDDTQKAAPANESSEAKNEP 144
                                                                                                                                                                                                                                                                                                                                                                          243 QKVDEHYANSLQNIAQKSLEBELDKATTNEQATQVK.NQFLENAQKLKEIQPLIKET---N 298
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               HSKLKQVVEDFRKKFFKTSEQVTPKKRLKRDLAANENNQQKIELTVSPENITVYEGEDVKF 418
                                                                                                                                  6 KNWAVVTLSTAALVFGATTVNASADTNIENNDSST-----VQVTTGDNDIAVKSVTLGS 59
                                                                                                                                                     -- 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----NVVKLGNKYYLFAATRLNRGSNDDAWMNANYAVGDNVAMVGYVADSLTGSYKPL- 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              571 ---NDSGVVLTASVPANWRTATYSYYAVPVAGKDDQ-----VLVTSYMTNRNGVAGKGM 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 679 QIVDDFDKKVEQDQPA------PIPENSEMDQAKEKAKIAVSKIMS------KVL 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGVHQ-----HLQKKNHSKIV------DLFKELEAIKQQTIFDIDNAKTEVEIDNLVH- 768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AGID----PNSLTDDQIKALNKMNFSKAAKSGTQMTYNDF----QKIAD--TLIKQDGRYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472 KS-----RATWAN----AAIGILKLNKDEKNPKVAELYSPLISAPMVSDEIERP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  622 DSTWAPSFLLQINPDNTTTVLAKMINQGDWIWDDSSENLDMIGDLDSAALPGERDKPVDW
                                                                                                                  Indels 259;
                                                                                         DB 4; Length 1098;
                                                                                                                                                                                                                                                                                                                                                                                                             232 VPFFKA-----SEIKNMPAATTKDAQTNTIEPLDVWDS-----
                                                                              Ouery Match
Best Local Similarity 19.2%; Pred. No. 5.3e-09;
Matches 179; Conservative 132; Mismatches 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNTPNTPEIPLTPETPKQPETQTNNRLPQT 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: amino acid
; TOPDLOGY: linear
; MOLECULE TYPE: protein
US-08-923-992A-8
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37; В 60 GQVSAAS------DTTIRTSANANSASSAANTQNSNSQVASSAAITS 100 Sequence 4, Application US/08923992A
Patent No. 6280738
GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IGA FC Binding Forms of the Group I UNMER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS: 101 ST-----SSAASLNNTDSKAAQENTNTAKNDDTQKAAPANESSEAKN 142 126 ETNRLLHIKQHEEVEKHNKPNQOKTLKQSDTKVDLSNIDKELNHQKSQVEAMAEQAGITN 185 143 EPAVNVNDSSAAKNDD-----QQSSKKNTTAKLNKDAENVVK------KAGID--- 184 ------PNSLIDDQIKALNKMNFSKAAKSGTQMTYNDF----QKI 219 220 AD--TLIKQDGRYTVPFFKA-----SEIKNMPAATTKDAQTNTIEPLDVWDS---- 264 Gaps 6 KNWAVVTLSTAALVFGATTVNASADTNIENNDSST-----VQVTTGDNDIAVKSVTLGS 59 235 QEHVKKETSSEENTQKVDEHYANSLQNLAQKSLEELDKATTNEQATQVK-NOFLENAQKL Length 1104; Indels 3: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, N.W., Suite 600 SOFTWARE: PATENTIN FLUOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,992A
FILING DATE: 05-SEP-1997
CLASSIFICATION: 536
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
NAMP: PATORNEY/AGENT INFORMATION: Ouery Match Best Local Similarity 19.6%; Pred. No. 8 1e-09; Matches 185; Conservative 129; Mismatches 351, 1438.0140001/RWE COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/POCKET NUMBER: 1438.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SED ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino acids Floppy disk ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-923-992A-4 COMPUTER READABLE FORM: STREET: 1100 mem amino acid USA MEDIUM TYPE: υ. Ω. ADDRESSEE: 20005 US-08-923-992A-4 COUNTRY: CITY: 1 STATE: 185 à g g ò q à ò q QQ δ

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294 KEIQPLIKET---NVKLYKAMSESLEQVEKELKHNSEANLQDLVAKSKEIVREYEGKLNQ 350
                                                                     351 SKNLPELKQLEEEAHSKLKQVVEHFRKKFKTSEQVTPKKRVKRDLAANENNQQKIELTVS 410
                                                                                                          MMGIPNQNDNHIYLLINKYGDNELSHWKNVGPIFGYNSTAVSQEWSGSAVLNSDNSIQLF 346
                                              ----WPVQDVRTGQVANWNGYQ----LVIA 286
                                                                                                                                                                             347 YTRVDTSDNNTNHQKIASATLYLTDNNGNVSLAQVRNDYIVF----EGDGYYYQTYDQWKA 403
                                                                                                                                                                                                        464 HKIABITIKNLKLNQSQTVTLKAKDDSGNV----VEKTFTITVQKKEEKQVPKTPEQ--K 517
                                                                                                                                                                                                                                                     TNKGADNIAMRDAHVIEDGNGDRYLVFEASTGLENYQGEDQIYNWLNYGGDDAFNIKSLF 463
                                                                                                                                                                                                                                                                                                                          RILSNDDIKS-----RATWAN------AAIGILKLNKDEKNPKVAELY------ 500
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                                                                                                                                                                                                                                                                                                                                                                                                  SPLISAPMYSDEIERPNYVKLGNKYYLFAATRLNRGSNDDAWMNANYAVGDNVAMYGYVA 560
                                                                                                                                                                                                                                                                                                                                                                                                                       617 NYQLHAQM---EILTRKVVQYMNKYPDNAEIKKIFESDWKRTKEDNYGSLENDALKGYFE 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSLTGSYKPL----NDSGVVLTASVPANWRTATYSYYAVPVAGKDDQ-----VLVTSYM 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             611 TNRNGVAGKGMDSTWAPSFLLQINPDNTTTVLAKMTNQCDWIWDDSSENLDMIGDLDSAA 670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     671 LPGERDKPVDWDLIG-----YGLK---PHDPATPNDPETPTTPETPETPNTPKTP 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-----KVLDGVHQ-----HLQKKNHSKIV------DLFKELEAIKQQTIFDIDNAK 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411 PENITVYEGEDVKFTVTAKSDSKTT--LDFSDLLTKYNPSVSDRISTNYKTNTDN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/07638431
Patent No. 5198535
GENERAL INFORMATION:
APPLICANT: Hoffman, Stephen L.
APPLICANT: Hedstrom, Richard
APPLICANT: Hedstrom, Richard
APPLICANT: Rogers IV, William O.
TITLE OF INVENTION: Protective malaria sporozoite surface protein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          718 KTPENPGTPQTPNTPPEIPLTPETPKQPETQTNNRLPQTGN 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: A. David Spevack
STREET: NMRDC Building 1 T-12 National Naval
STREET: Medical Center
CITY: Bethesda
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALCHIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/638,431
FILING DATE: 19910110
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                95 LIKLK------GYGSTSKDSLRFILAHLQNNYSPNGNTNLTSALLVVDTLINBRMYRP 146
                                                                                                                                                                                                                                                                                                                                                                                               517 NYVKLGNKYYLFAATRLNRGSNDDAWMNANYAVGD-----NYAMVGYVADSLTGSYK- 568
                                                                                                                                                                                                                                                                                                                                                                                                                      569 ------PLNDSGVVLTASVPANWRTATYSYYAVPVAGKDDQVLVTSYMTNRNGVA 617
                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              703 TTPETPETPNTPKTPKTPENPGTPQTPNTPNTPEIPLTPETPKQPETQTNNRLPQTGNNA 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    470 DIKSRATWANAAIGILKLNKDEKNPKVAEL---YSP------LISAPMVSDEIERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 ILVGCDRYAPCPYYSSG-----SWNEA------QNMIKPFLT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------MIGDLDSAAL------PGERDKPVDWDLIGYGLKPHDPATPNDPETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        618 GKGMDSTWAPSFLLQINPDNTTTVLAKMTNQGDW-IWDDSSENLD-------
                                                                                                                                                                                                             5.3%; Score 220; DB 1; Length 826;
20.7%; Pred. No. 1.1e-07;
Live 46; Mismatches 132; Indels 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: September 21, 2002, 23:37:39
Job time: 5080 sec
   NAME: Spewack, Avrom D.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-6759
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 826 antho acids
TYPE: AMINO ACID
INFORMATION:
                                                                                                                                                                                                        Query Match 5.3°
Best Local Similarity 20.7°
Matches 87; Conservative
                                                                                                                                                / MOLECULE TYPE: protein US-07-638-431-2
                                                                                                                                      linear
                                                                                                                               TOPOLOGY:
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BG441163 GA_Ea001
AL004959 F. rubripe
AL130699 Fugu rubr
AZ185454 SP_1005_A
BG226324 Kq20c02.y
BH138523 ENTOBOTR
BH211305 Sm1-50G22
AZ204694 SP_0100_A
BH203231 Sm1-57813
AU179547 AU179547
AL019712 F. rubripe
AL4425 Fugu rubr
AQ411051 CpG0931A
AL065406 Drosophil
BE124644 EST393649
BG447645 RF0334125
AZ542140 ENTEW36TF
AU180091 AU180091
                                                                                                                                                                                                                                                                                                                                    290761 F.rubilpes
AL051540 Drosophil
AI443192 sa45f05.y
AI496419 sb04e01.y
BF95475 su77f03.y
BE020655 sm51h06.y
A2183618 SP_1001_A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jacobanda 11 - MAY - 2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 139021 of library G from Tetraodon nigroviridis, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS; genome survey sequence.

Tetracdon nigroviridis.
Tetracdon nigroviridis.
Tetracdon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Acatinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acatthomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes;
Tetracdontidae; Tetracdon.
1 (bases 1 to 989)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Metassenbach,J. and connet analysis of the commant analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases I to 989)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Characerization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome. For more information, project or use a http://www.genoscope.cns.fr/Tetraodon. Location/Qualifiers 1. 989 /organism="Tetraodon nigroviridis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                 BH138523
BH211305
BH211305
BH203231
AU179547
FR0026883
FR0047466
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AL44458 Fugu rubr
AL299119 Terracedon
AL444858 Fugu rubr
AL018519 F.rubripe
AL011359 F.rubripe
290754 F.rubripes
AL281759 Terracedon
AL44288 Fugu rubr
AL94286 Drosophil
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AL44286 Fugu rubr
AL44386 Fugu rubr
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                          nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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FR005944
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Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
1 (bases 1 to 501)
Clark, M.S.
                                          ID : COAG139AH11LP1~end : T7"
t 41 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CBIO ISB. UK Email: biohelp@hgmp.mrc.ac.uk
                                                                                                                                        63 tgcaacaactgtaaatgcatccgcggacacaaatattgaaaacaatgattctctactgt 122
                                                                                                                                                                                      acaagttacaacaggtgataatgatattgctgttaaaagtgtgacacttggtagtggtca 182
                                                                                                                                                                                                                                  183 agttagtgcagctagtgatacgactattagaacttctgctaatgcaaatagtgcttcttc 242
                                                                                                                                                      tacaagttccgcagcttcattaaataacacagatagtaaagcggctcaagaaaatactaa 362
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The BACs can be obtained from http://www.incyte.com.
Location/Qualifiers
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Fugu rubripes GSS sequence, clone 264E22cA9, genomic survey
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m
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48.9%; Pred. No. 1.7e-07;
ative 8; Mismatches 213; Indels 3
                                                      41 others
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g 261
/db_xref="taxon:99883"
/clone="139021"
/clone_lib="G"
/note="Genoscope sequenc
a 245 c 122 g 28
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Tetracdon nigroviridis genome survey sequence T7 end of clone
123M05 of library G from Tetracdon nigroviridis, genomic survey
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Tetraodontidae: Tetraodon.

Tobases 1 to 735;

Rost-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Weissenbach, J.

Meissenbach, J.

Meissenbach, J.

Meraterization and repeat analysis of the compact genome of the Ireshvater pufferfish Tetraodon nigroviridis
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Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                        57 atttggtgcaacaactgtaaatgcatccgcggacacaaatattgaaaacaatgattcttc 116
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al Similarity 48.18; Pred. No. 1.8e-06;
216; Conservative 0; Mismatches 233;
1. .501
/organia="nakifugu rubripes"
/db_xref="taxon:31033"
/clone="264E22cA9"
/clone_lib="BAC_264E22"
2 a l61 c 35 g 173 t
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GSS; genome survey sequence.
Tetraodon nigroviridis.
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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GSS; genome survey sequence.
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Actinopterygii, Medazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Acanthopterygii; Teleostei; Medeleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
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28 others
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/db_xref="taxon:99883"
/clone="123M05"
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Pred. No. 3e-06;
8; Mismatches 219;
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                       3 (bases 1 to 735)
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                                   AUTHORS
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Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clonne-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                   2 (bases 1 to 773)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
              Fisher, C.,
                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence ID : COAG199BB12LP1~end : T7*
9 184 t 45 others
Roest Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
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                                                            Charaterization and repeat analysis of the compact genome freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 ttacactctcgactgctggctggtatttggtgcaacaactgtaaatgcatccgcggaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ctgttaaaaagtgtgacacttggtagtggtcaagttagtgcagctagtgatacgactatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 gaacttctgctaatgcaaatagtgcttcttctgccgctaatacacaaaattctaacagtc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="199024"
/clone=lib="G"
/note="Genoscope sequence ID : COA
note="Genoscope sequence ID : COA
note="Genoscope sequence ID : COA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.2%; Score 74.8; DB 12;
42.0%; Pred. No. 4.1e-06;
ative 34; Mismatches 241;
                                                                                                                                                                                                                                                                (bases 1 to 773)
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FR0048073
LOCUS
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GSS 05-JAN-2001

linear

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FR0048073

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                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Tetraodontideostei; Tetraodontideostei; Tetraodontideostei; Tetraodontideostei; Tetraodontideostei; Tetraodontideostei; Tetraodontideostei; Tetraodontideostei; Tetraodontideostei; Sa Clark, M.S.

Salark, M.S.

Direct Submission

L. Submitted (19-SEP-2000) MRC Human Genome Mapping Project Resource biohelpehagn-mc.ac.uk
Vector: pBluescript II KS
V-type: phagemid
PRIMER: KS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 gtgtgacacttggtagtggtcaagttagtgcagctagtgatacgactattagaacttctg 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          400
                                                                                                                                                                                                                                                                                            One pass dye-terminator sequencing of BAC (pBeloBACII) cloned genomic sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341 aagoggottoaagaaaatactaatacagoccaaaaatgatgacacgcaaaaagctgcaccag
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Location/Qualifiers
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        clone 263K15bD8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.1%; Score 72.6; DB 12;
48.2%; Pred. No. 1.1e-05;
tive 0; Mismatches 219;
                                                                                                                                                                                                                                                                                                                                                             /organism="Takifugu rubripes"
/db xref="taxon:31033"
/clone="258185b08"
/clone="1b="88455"
163 c 45 g 158 t
                                            AL444858.1 GI:12052694
GSS; genome survey sequence.
Takifugu rubripes.
Takifugu rubripes
Fugu rubripes GSS sequence,
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                sequence.
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AL444858.1 G
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Matches 204;
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RESULT 6 FR0025683

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450 bp DNA linear GSS 10-DEC-1997 clone 154E17aCl2, genomic survey sequence.
                                                                                                               Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Taxifugu.

1 (bases 1 to 450)

1 (bases 1 to 450)

Williams, G. and Brenner, S., Meek, S., Warner, S., Umrania, Y., Direct Submission

Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CBIO 15B. Email: biohelp@hgmp.mrc.ac.uk
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Takifugu rubripes.
Takifugu rubripes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
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Similarity 50.1%; Pred. No. 1.6e-05;
%; Conservative 0; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone_lib="cosmid 154E17"
/clone="154E17aC12"
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                                                               GSS; genome survey sequence.
Takifugu rubripes.
Takifugu rubripes
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                     GSS sequence,
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                                                     AL018519.1 GI:2684887
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                  F.rubripes
AL018519
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Best Local Simi
Matches 178;
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FR0018463/c
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Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae: Taxifugu.

1 (bases 1 to 470)

Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y., Willidams,G. and Brenner,S.
Direct Submission
Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Vector: pBluescript II KS
V_type: phagemid
PRIMER: KS
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1 (Bases 1 to 619)
Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y., Millams,G. and Brenner,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        619 bp DNA linear GSS 02-MAR-199
clone 133B16aC7, genomic survey sequence.
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48.6%; Pred. No. 0.0001;
tive 0; Mismatches 179; Indels 0
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CNSO4AEE 806 bp DNA linear GSS 21-MAY-2000 Tetracodon nigroviridis genome survey sequence T7 end of clone 095G24 of library G from Tetracodon nigroviridis, genomic survey
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Roest Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Weissenbach, J.
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Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
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                                                   One pass dye-terminator sequencing of cosmid cloned genomic
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2.8%; Score 67.2; DB 12; Length
Best Local Similarity 48.3%; Pred. No. 0.00018;
Matches 174; Conservative 0; Mismatches 186; Indels
                                                                                         Location/Qualifiers
1. 619
/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone_lib="cosmid l33B16"
/clone="133B16aC7"
a 150 c 116 g 175 t
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AL281759.1 GI:8020086
GSS; genome survey sequence.
Tetraodon nigroviridis.
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                    Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This Sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetracdon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.

http://www.genoscope.cns.fr/Tetracdon.

Location/Qualifiers
L. 806
//Organism="Tetracdon nigroviridis"
//db_xref='taxon:99883"
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AL062806.1 GI:4943996
GSS.
                                                                                                                                                                                          : C0BG095BD12LP1~end : T7"
40 others
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41.3%; Pred. No. 0.0002;
iive 29; Mismatches 289;
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  (bases 1 to 806)
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Matches 224; Conservative
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
- Web : www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of collaboration with the BAC-end sequence was carried out as part of a release permination of the Bocsephila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Prosophila haron melanogaster BAC library was prepared by Kazutcyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, BY. The library is named RPCI-98 and was constructed by partial isogenic strain v2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library filters for Mybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera: Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xxef="texon:7227"
/clone_lib="RPCI-98"
/clone="BACRI3F18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.8%; Score 65.6; DB 12; Best Local Similarity 31.9%; Pred. No. 0.00046; Matches 210; Conservative 111; Mismatches 337;
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63 c 52 g
                                                                                           1 (bases 1 to 959)
Genoscope.
                                                                                                                                                       Direct Submission
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GSS 05-JAN-2001
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1 (bases 1 to 619)
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                                                                                                                                                                                                                                                                                                                                                                                            Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. UK Email:
biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
771 acctttagatgtatgggattcatggccagttcaagatgttcggacaggacaagttgctaa 830
                  acaactgtaaatgcatccgcggacacaaatattgaaaacaatgattcttctactgtacaa 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 gttacaacaggtgataatgatattgctgttaaaagtgtgacacttggtagtggtcaagtt 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                891 tatctatctcttatataaataagtatggtgataatgaattaagtcattggaagaatgta 948
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                                                                                                                     Gaps
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Fugu rubripes GSS sequence, clone 217A13gF11, genomic survey
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Pred. No. 0.00092;
0; Mismatches 140; Indels
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/db_xref="taxon:31033"
/clone="217A13gF11"
/clone_11b="BAC 217A13"
161 130 g 143 t
                                                                                                                                                                                                                                                            GSS; genome survey sequence.
Takifugu rubripes.
Takifugu rubripes
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PRIMER: KS
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Matches 142;
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VERSION
KEYWORDS
SOURCE
ORGANISM
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FR0047503
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DEFINITION
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EST 09-JAN-2002
                                                                                                                                               Gossyplum arborcum.
Gossyplum arborcum.
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossyplum.

1 (bases 1 to 698); Malvales; Malvaceae; Gossyplum.

Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, An integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
                                 ьмээв6в9
698 bp mRNA linear EST 09-JAN-200;
arboreum cDNA clone GA_Ea0011P05r, mRNA sequence.
BM338689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:29729"
/dlone="GA_Ea0011P05r"
/clone=1lb="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2064 aaaaccgcatgatcctgctacaccaaatgatcctgaaacgccaactacaccagaaaccc 2123
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171 c 154 g 122 t
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Pred. No. 0.0012;
0; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                 100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. 698
/organism="Gossypium arboreum"
                                                                                                                                                                                                                                                                                                                                                                                                                   Email: rwing@clemson.edu
Total High Quality bases - 449
Seq primer: RAATAGGACTGATARGGG
High quality sequence start: 4
High quality sequence stop: 550.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cultivar="8400"
                                                                                                 BM358689.1 GI:18099435
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                                                                                                                                    Gossypium arboreum
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108; Conservative
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Best Local
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 12
                                 LOCUS
DEFINITION
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CNSO6PDW/c
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ORIGIN
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CNSO6PDW 979 bp 'DNA linear GSS 05-JUL-2001 T7 end of clone AV0AA013G05 of library AV0AA from strain CBS 379 of

LOCUS

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429 accagctgtaaacgttaatgattcttcagctgc 461
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Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue daston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

2 rue daston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

Location/Qualifiers
irce

1. 979
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                                                                                                                Saccharomycetes;
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Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,B.,
Wincker,P. and Welssenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
PEBS Lett, 487 (1), 3-12 (2000)
                                                                                                                                                 Bon, E., Neuveglise, C., Lepingle, A., Wincker, P., Artiguenave, F., Gaillardin, C. and Casaregola, S. Genomic exploration of the hemiascomycetous yeasts: 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 tctactgtacaagttacaacaggtgataatgatattgctgttaaaagtgtgacacttggt 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 ACAACCACTACAGGAACTGGTGCAACCGATGGTAATGGTTCTCAAAGTACAACTGATGGT 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 gcttcttctgccgctaatacacaaaattctaacagtcaagtagcaagttctgctgcaata 294
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                                                                                 Saccharomyces exiguus
Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Pred. No. 0.0013;
0; Mismatches 174; Indels
Saccharomyces exiguus, genomic survey seguence.
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                                                                                                                                                                                                      Saccharomyces exiguus
FEBS Lett. 487 (1), 42-46 (2000)
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/clone_lib="Av0AA"
/note="end : T7"
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                                AL409242.1 GI:12176588
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Matches 168; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 ISB. UK Email:
biohelp@Hgmp.mrc.ac.uk
Vector: pBluescript II KS
                      acatcatctacaagttccgcagcttcattaaataacacagatagtaaagcggctcaagaa 354
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Fugu rubripes GSS sequence, clone 217A131G11, genomic survey
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Pred. No. 0.0013;
0; Mismatches 176; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic sequence
The BACs can be obtained from http://www.incyte.com.
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                                                                      355 aatactaatacagccaaaaatgatgacacgcaaaaagctgca 396
                                                                                             1. .619
/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone="217A13iG11"
/clone="11b="BAC_217A13"
2 a 172 c 92 g 177 t
                                                                                                                                                                                                                                                                    AL444386
AL444386.1 GI:1205222
GSS; genome survey sequence.
Takifugu rubripes
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Best Local Similarity 47.19
Matches 157, Conservative
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us-09-995-587a-2.rst

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Trypanosoma.

Trypanosoma.

Trypanosoma.

Trypanosoma.

E. Sayed, N., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J. Prascr. C. and Adams, M.

Determination of Clone end sequences from Trypanosoma brucei GuTat 10.1 sheared DNA library

Unpublished (1999)

Other_GSSs: Sheared DNA-46723.TF

Contact: Najib M. El-Sayed

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Fax: 301 838 0200

Fax: 301 838 0200
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/db_xref="taxon:5691"
/clone="sheared DAA46/23"
/clone="Sheared DAA46/23"
/clone="Sheared DAA46/23"
/clone="Sheared DAA;"
/note="Vector: pUC18; Site=1: Smal; Constructed at The Institute for Genomic Research (TIGR). Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma bruce; (TRED/92/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999):"
                                                                                                                           AQ946120 641 bp DNA linear GSS 27-JAN-2000 Sheared DNA-46J23.TR Sheared DNA Trypanosoma brucel genomic clone Sheared DNA-46J23, DNA sequence.
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Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TiGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: M13-Reverse
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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309 TACTGCTGNTACTNCTACTNCTACGGCTNC 341
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345 ggctcaagaaaatactaatacagccaaaaatgatgacacgcaaaaagctgcaccagctaa 404
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                                                                                                                     525 aaacgttgtaaaaaaggcgggaattgatcctaacagtttaactgatgaccagattaaagc 584
                                                                                                                                         405 cgaatcttctgaagctaaaaatgaaccagctgtaaacgttaatgattcttcagctgcaaa
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Sequence 1
Sequence 1
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APPLICANT: Hiroaki Tanaka
TITLE OF INVENTION: High Throughput DNA sequencing vector
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Homology with X06404 compl (411..1668)
LOCATION: 9..1266
IDENTIFICATION METHOD: blastn against X06404
                                                       US-08-928-3618-4
US-08-700-651-2
US-08-700-651-2
US-08-700-651-2
US-08-705-4
US-08-795-475-4
US-08-95-475-4
US-08-961-083-159
US-08-961-083-159
US-08-257-073-14
US-08-559-8968-1
US-08-557-073-10
US-08-928-3618-2
US-08-928-3618-2
US-08-928-3618-1
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CURRENT APPLICATION DATA:
PPLLING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ISRABISEN: 09,655
REFERENCE/DOCKET NUMBER: 29,655
REFERENCE/DOCKET NUMBER: 6ENSET.015A
TELECHONEN: (619) 235-6176
INFORMATION: (619) 235-6176
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TEMETER OF SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Patent No. 6022716
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: Win95
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TOPOLOGY: CIRCULAR
MOLECULE TYPE: Synthetic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
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NUCLEIC ACID
EDNESS: DOUBLE
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STATE: California
            US-09-058-746-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Al
Sequence 5, Al
Sequence 14, 2
Sequence 1, Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Sequence 5, Sequence 9, Sequence 1, Sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1,
Sequence 8,
Sequence 8,
Sequence 8,
Sequence 1,
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Sequence 3
Sequence 5
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued_Patents_NA:*
l: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
! /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
! /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
! /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
! /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
! /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
! /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08 - 242 - 912 - 8

US-08 - 714 - 481 - 8

US-08 - 714 - 481 - 8

US-08 - 906 - 06111 - 8

US-08 - 923 - 992A - 7

US-08 - 923 - 992A - 5

US-08 - 923 - 992A - 5

US-08 - 923 - 992A - 9

US-08 - 923 - 992A - 9

US-08 - 923 - 992A - 9

US-08 - 923 - 992A - 1

US-08 - 923 - 922A - 1

US-08 - 923 - 923 - 14

US-08 - 870 - 827 - 4

US-08 - 870 - 827 - 4

US-08 - 923 - 323A - 1

US-08 - 770 - 379 - 20

US-08 - 770 - 379 - 20

US-08 - 923 - 371A - 20

US-08 - 682 - 517 - 14

US-08 - 682 - 517 - 14
                                                                                                                                                                                                                                                                                                                                                                                                    383533 segs, 122816752 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                   OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                    US-09-995-587A-2
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                    Run on:
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NAME/KEY: Homology with J01688 (complement 175..819)
LOCATION: 6574..7218
IDENTIFICATION METHOD: blastn against J01688
OTHER INFORMATION: mutation A -> G 7096
                                                                                                                                                                                                                                                NAME/KEY: single stranded DNA replication origin
LOCATION: 1423..1894
IDENTIFICATION METHOD: By homology to U46017
OTHER INFORMATION: mutation T -> C 1658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: IncC
LOCATION: 3070..3320
IDENTIFICATION METHOD: By homology to U51113
OTHER INFORMATION: insertion 33 bases 3038..3071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS streptomycin sensitivity gene LOCATION: complement 6716..7090
IDENTIFICATION METHOD: By homology to J01688 OTHER INFORMATION: mutation A -> 6 6728
OTHER INFORMATION: mutation G -> C 6821
OTHER INFORMATION: mutation C -> T 6866
OTHER INFORMATION: mutation T -> C 7013
FEATURE:
NAME/KEY: rpslR
                                                            NAME, KEY: Th1000's right end LOCATION: complement 1332..1371
IDENTIFICATION METHOD: blastn against x60200)
                                                                                                                                                    NAME/KEX: Homology with U46017 (1-472)
LOCATION: 1423.1894
IDENTIFICATION METHOD: blastn against U46017
LOCATION: 142..957
IDENTIFICATION METHOD: By homology to X06404
                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Homology with U51113 (2382..6997)
LOCATION: 1896..6544
IDENTIFICATION METHOD: blastn against U51113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              By homology to U51113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: ParA
LOCATION: 3655.4821
IDENTIFICATION METHOD: By homology to U51113
OTHER INFORMATION: mutation G -> A 3878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               By homology to U51113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 4821..5792
IDENTIFICATION METHOD: By homology to U51113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: ParC
LOCATION: 5865..6382
IDENTIFICATION METHOD: By homology to U51113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEX: repELR
LOCATION: 2897..2918
OTHER INFORMATION: Described in seqID 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: LRT3RA
LOCATION: complement 3045..3069
OTHER INFORMATION: Described in seqID 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: T3
LOCATION: 3043..3059
OTHER INFORMATION: Described in seqID 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: OriS
LOCATION: 1972..2188
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: RepE
LOCATION: 2903.3034
IDENTIFICATION METHOD:
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NAME/KEY: ParB
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NAME/KEY: high copy-number double-stranded DNA replication origin LOCATION: complement 9629.10315
IDENTIFICATION WETHOD: By homology to M77789
OTHER INFORMATION: mutation C -> T 9803
OTHER INFORMATION: site Scal 10029 - 10034
OTHER INFORMATION: site Pml1 10038 - 10043
OTHER INFORMATION: CLONING SITES 10031 - 10041
                                                                                                                                                                                                                                                                                                                                                                          FEATURE:

NAME/KEY:
CDS levansucrase gene
LOCATION: complement 7379.8800

LDENTIFICATION METHOD: By homology to X02730

OTHER INFORMATION: mutation 7 -> C 7466

OTHER INFORMATION: mutation 7 -> C 7467

OTHER INFORMATION: mutation 7 -> C (Asn -> Asp) 8347

OTHER INFORMATION: mutation 7 -> C (Asn -> Asp) 8347

OTHER INFORMATION: mutation 7 -> C (Asn -> Asp) 8347

OTHER INFORMATION: mutation 6 -> A (Ala -> Val) 8772

NAME/KEY: SLR3

LOCATION: 8711..8731

OTHER INFORMATION: Described in seqID 14

FEATURE:
NAME/KEY: Homology with J01636 (complement 1158..1465)
LOCATION: 9298..9633

IDENTIFICATION METHOD: blastn against J01636
                                                                                                                                                                                                                                                                             NAME/KEY: Homology with X02730 (complement 37.1959) LOCATION: 7305.9227 IDENTIFICATION METHOD: blastn against X02730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
CDS alpha peptide beta-galactosidase
LOCATION:
COMPLEMENT 9276..9497
FEATURE:
NAME/KEY:
PATURE:
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LOCATION: 9629..10315
IDENTIFICATION METHOD: blastn against M77789
LOCATION: 7155..7174
OTHER INFORMATION: Described in seqID 12
                                                                         NAME/KEY: SP6
LOCATION: 7230..7248
OTHER INFORMATION: Described in seqID 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: OS1
LOCATION: 10009..10026
OTHER INFORMATION: Described in seqID 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement 10046..10062
WATION: Described in seqID 11
                                                                                                                                                FEATURE:
NAME/KEY: Tn1000's left end
LOCATION: 7252..7291
IDENTIFICATION METHOD: blast (X60200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE: CLONING SITES 1003
NAME/KEY: OriLRd
COCATION: 9856..9881
OTHER INFORMATION: Described in seqID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer LacLRS2Avr
complement 9603..9630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer LacE2Mlu
9289..9314
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LOCATION: COMpleme
OTHER INFORMATION:
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LOCATION:
FEATURE:
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LOCATION:
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NAME/KEY: OriLRr

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9
                                                                                       1043 caagggtagacacgictgataacaataccaatcatcaaaaaattgctagcgctactctt 1102
                                                                                                                                           8262 C-----TGATTICTCCGGTAAACATTACGGCAAACAACAACTGACAACTGCAAACTGACAAGTTA 8209
                                                                                                                                                                      1103 atttaactgataataatggaaatgtatcactcgctcaggtacgaaatgactatattgtat 1162
                                                                                                                                                                                                               8148 TTGACGGTGACGGAAAAACGTATCAAAATGTACAGCAGTTCATCGATGAAGGCAACTACA 8089
                                                                                                                                                                                                                                                        1220 gtgccgataatattgcaatgcgtgatgctcatgtaattgaagatggtaatggtgatcggt 1279
                                                                                                                                                                                                                                                                     1280 accttgtttttgaagcaagtactggtttggaaattatcaaggcgaggaccaaatttata 1339
                                                                                                                                                                                                                                                                                                                                       1340 actggttaaattatggcggagatgacgcatttaatatcaagagcttatttagaattctt 1399
                                                                                                                                                                                                                                                                                                                                                          1968 TTAACAAAGCATACTATGGCAAAAGCACATCATTCTTCCGTCAAGAAAGTCAAAAACTTC 7909
                                                                                                                                                                                                                                                                                                                                                                                                                     1400 ccaatgatgatattaagagtcgggcaacttgggctaatgcagctatcggtatcctcaaac 1459
                                                                                                                                                                                                                                                                                                                                                                                            7848 TAAACGATGATTACACACTGAAAAAGTGATGAA-----ACCGCTGATTGCATCTA 7798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1580 tatttgccgctacccgtttaaatcgaggaagtaatgatgatggtggatgatgctaatt 1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7737 İGITCACIGACICCCGCGGAICAAAAIGACGAIIGACGGCAIIACGICIAACGAIAII 7678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1700 ataagccattaaatgattctggagtagtcttgactgcttctgttcctgcaaactggcgga 1759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7638 ACAAGCCCCTGAACAAAACTGGCCTTGTGTTAAAAATGGATCTTGATCCTAACGATGTAA 7579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cagcaacttattcatattatgctgtccccgttgccggaaaagatgaccaagtattagtta 1819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cttcatatatgactaatagaaatggagtagcgggtaaaggaatggattcaacttgggcac 1879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
                                              Owery Match
Best Local Similarity 47.7%; Pred. No. 4e-11;
Matches 464; Conservative 0; Mismatches 460; Indels 46
CCATION: complement 10182..10202

19-09-058-746.1

US-09-058-746.1
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APPLICANT: Ilya Chumakov
APPLICANT: Hiroaki Tanaka
AITLE OR INVENTION: High Throughput DNA equencing vector
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homology with X06404 compl (411..1668)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: single stranded DNA replication origin LOCATION: 1423..1894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Tn1000'sright end
LOCATION: complement 1332..1371
IDENTIFICATION METHOD: blastn against X60200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Kanamycin resistance gene CDS
LOCATION: 142.957
IDENTIFICATION METHOD: By homology to X06404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION METHOD: blastn against X06404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1423..1894
IDENTIFICATION METHOD: blastn against U46017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1423..1894
IDENTIFICATION METHOD: By homology to U46017
OTHER INFORMATION: mutation T -> C 1658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Homology with U51113 (2382..6997)
LOCATION: 1896..6544
IDENTIFICATION METHOD: blastn against U51113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Homology with U46017 (1-472)
LOCATION: 1423..1894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENSET.015C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Cloning vector pGenDEL
                                                                                                                                       Sequence 1, Application US/09438142; Patent No. 6258571; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: Win95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: GER
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (619) 235-8550
TELEPAX: (619) 235-8550
TELEFAX: (619) 235-0176
SEQUENCE CHARACTERISTICS:
LENGTH: 10317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: circular
MOLECULE TYPE: synthetic DNA
ORIGINAL SOURCE:
1940 atcaaggggatt 1951
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                         7407 AACAAGGACAAT 7396
                                                                                                                                                                                                                                                                                                                                                    CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pGendel
1..10317
                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 92101-3505
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                                                                                                    RESULT 2
US-09-438-142-1/C
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us-09-995-587a-2.rni

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NAME/KEY: Homology with J01688 (complement 175..819)
LOCATION: 6574..7218
IDENTIFICATION METHOD: blastn against J01688
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NAME/KEX: Homology with X02730 (complement 37..1959)
LOCATION: 7305..9227
IDENTIFICATION METHOD: blastn against X02730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: IncC
LOCATION: 3070..3320
IDENTIFICATION METHOD: By homology to U51113
OTHER INFORMATION: insertion 33 bases 3038..3071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS streptomycin sensitivity gene LOCATION: complement 6716.7090
IDBNTIFICATION METHOD: By homology to J01688 OTHER INFORMATION: mutation A -> G 6728 OTHER INFORMATION: mutation G -> C 6821 OTHER INFORMATION: mutation T -> T 6866 OTHER INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: mutation T -> A 7058 NAME/KEY: FPSIRE INFORMATION: MUTATION:                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: RepE
LOCATION: 2903.3034
IDENTIFICATION METHOD: By homology to U51113
                                                                                                                                              By homology to U51113
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LOCATION: 3655..4821
IDENTIFICATION METHOD: By homology to U51113
OTHER INFORMATION: mutation G -> A 3878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: ParC
LOCATION: 5865..6382
IDENTIFICATION METHOD: By homology to U51113
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IDENTIFICATION METHOD: By homology to US1113
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LOCATION: complement 7379..8800
IDENTIFICATION METHOD: By homology to X02730
OTHER INFORMATION: mutation T -> C 7466
                                                                                                                                                            FEATURE:
NAME/KEY: reperR
LOCATION: 2897..2918
OTHER INFORMATION: Described in seqID 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME, KEX: T3
LOCATION: 3043..3059
OTHER INFORMATION: Described in seqID 17
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OTHER INFORMATION: Described in seqID 15
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LOCATION: 7230..7248
OTHER INFORMATION: Described in seqID 13
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OTHER INFORMATION: Described in seqID
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LOCATION: 7252..7291
LDENTIFICATION METHOD: blast (X60200)
FEATURE:
NAME/KEY: Or1S
LOCATION: 1972..2188
IDENTIFICATION METHOD:
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8262 C----TGATTTCTCCGGTAAACATTACGGCAAACAACACTGACAACTGCACAAGTTA 8209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 1103 atttaactgataatggaaatgtatcactccgctcaggtacgaaatgactatattgtat | 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: high copy-number double-stranded DNA replication origin LOCATION: complement 9629.10315
IDENTIFICATION METHOD: By homology to M77789
OTHER INFORMATION: mutation C -> 7 9803
OTHER INFORMATION: site Scal 10029 - 10034
OTHER INFORMATION: site Pml1 10039
OTHER INFORMATION: CLONING SITES 10031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
3.4%; Score 80; DB 4; Length 10317;
Best Local Similarity 47.7%; Pred. No. 4e-11;
Matches 464; Conservative 0; Mismatches 460; Indels 48;
                                                                                                                                                                                    NAME/KEY: Homology with J01636 (complement 1158..1465)
LOCATION: 9298..9623
    mutation A -> G 7739 mutation T -> C (Asn -> Asp) 8347 mutation T -> C 8600 mutation G -> A (Ala -> Val) 8772
                                                                                                                                                                                                                                                                   NAME/KEY: CDS alpha peptide beta-galactosidase LOCATION: complement 9276..9497
IDENTIFICATION METHOD: BY homology to J01636
FEATURE:
                                                                                                                                                                                                                       IDENTIFICATION METHOD: blastn against J01636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Homology with M7789 (1889..2576)
LOCATION: 9629..10315
IDENTIFICATION METHOD: blastn against M77789
                                                                                                NAME/KEY: SLR3
LOCATION: 8711..8731
OTHER INFORMATION: Described in seqID 14
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OTHER INFORMATION: Described in seqID 10
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OTHER INFORMATION: Described in seqID 11
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LOCATION: Complement 10182..10202
; GTHER INFORMATION: Described in seqID 9
US-09-438-142-1
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LOCATION: 9856..9881
OTHER INFORMATION: Described in seqID
                                                                                                                                                                                                                                                                                                                                                      primer HE1
complement 9465..9479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer LacLRS2Avr
complement 9603..9630
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9289..9314
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9461..9475
OTHER INFORMATION:
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LOCATION:
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LOCATION:
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1163 tigaaaggiga iggotattactaccaaacttaiga icaaigga---aagctactaacaaag 1219
                                                8148 TTGACGGTGACGGAAAAACGTATCAAAATGTACAGCAGTTCATCGATGAAGGCAACTACA 8089
                                                                                                                           1280 accttgtttttgaagcaagtactggtttggaaaattatcaaggcgaggaccaaatttata 1339
                                                                                                                                             8028 ACTTAGTATTTGAAGCAAACACTGGAACTGAAGATGGCTACCAAGGGGAAGAATCTTTAT 7969
                                                                                                                                                                             1340 actggttaaattatggcggagatgacgcatttaatatcaagagcttatttagaattctt 1399
                                                                                                                                                                                                      7968 TTAACAAAGCATACTATGGCAAAAGCACATCATTCTTCCGTCAAGAAAGTCAAAAACTTC 7909
                                                                                                                                                                                                                                                   1460 taaataaggacgaaaagaatcctaaggtggcagagttatactcaccattaatttctgcac 1519
                                                                                                                                                                                                                                                                                                  1520 caatggtaagcgatgaaattgagcgaccaaatgtagttaaattaggtaataaattact 1579
                                                                                                                                                                                                                                                                                                                                                   1580 tattigccgctacccgtttaaatcgaggaagtaatgatgatgcttggatgatgctaatt 1639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1700 ataagccattaaatgattctggagtagtcttgactgcttctgttcctgcaaactggcgga 1759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7638 ACAAGCCGCTGAACAAAACTGGCCTTGTGTTAAAAATGGATCTTGATCCTAACGATGTAA 7579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1760 cagcaacttattcatattatgctgtcccgttgccggaaaagatgaccaagtattagtta 1819
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Patent No. 5595740
GENERAL INFORMATION:
APPLICANT: Brady, L. Jeannine
TITLE OF INVENTION: Cloning of No. 5595740-IgA FC Binding Forms of TITLE OF INVENTION: the Group B Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                              1400 ccaatgatgatattaagagtcgggcaacttgggctaatgcagctatcggtatcctcaaac
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2421 N.W. 41st Street, Suite A-1
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APPLICANT: Brady, L. Jeannine
TITLE OF INVENTION: Cloning of No. 5766606-1gA FC Binding Forms of
TITLE OF INVENTION: the Group B Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2669 CGTGTTCCGGAATCACCAAAGACTCCAGAAGGCGCATGTTCCGGAATCACCAAAGACT
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              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
SPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,932
FILING DATE: 16-MY-1994
CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saltwanchik, David R.
REGISTRATION NUMBER: 31,794
DEPREDENT FORCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 APPLICATION DATA:
APPLICATION NUMBER: US/08/714,481
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2.9%; Score 68.8; DB 1;
Best Local Similarity 60.9%; Pred. No. 2.1e-08;
Matches 112; Conservative 0; Mismatches 7;
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STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08714481
Patent No. 5766606
                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: DNA (genomic) US-08-242-932-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                        LENGTH: 3730 base pairs
TYPE: nucleic acid
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                        linear
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2065 aaaccgcatgatcctgctacaccaaatgatcctgaaacgccaactacaccagaaaccct 2124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2669 CGTGTTCCGGAATCACCAAAGACTCCAGAAGCACCGCATGTTCCGGAATCACCAAAGACT 2728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
2.9%; Score 68.8; DB 5; Length 3730;
Best Local Similarity 60.9%; Pred. No. 2.1e-08;
Matches 112; Conservative 0; Mismatches 72; Indels 0
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Fatent No. 6048694
GENERAL INFORMATION:
APPLICANT: MICHAEL GENE BRAMUCCI
APPLICANT: VASANTHA NAGARAJAN
ITILE OF INVENTION: POSITIVE SELECTION
ITILE OF INVENTION: VECTOR FOR BACILLUS SP.
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: E. I. DU PONT DE NEMOURS AND ADDRESSEE: COMPANY
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MEDIUM TYPE: DISKETTE, 3.5 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT OFFICE 97
                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
RECISTRATION NUMBER: 31,794
REPERENCE/DCKET NUMBER: UF142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
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APPLICATION NUMBER: US/09/068,043
                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-06111-8
                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: L'ENGTH: 3730 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: NOVEMBER 3, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                             LENGTH: 3730 Dasc TYPE: nucleic acid
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US-09-068-043-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2669 CGTGTTCCGGAATCACCAAAGACTCCAGAAGCACCGCATGTTCCGGAATCACCAAAGACT 2728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2185 cctaatacacctaatactccggaaattcctttaactccagaaacgcctaagcaacctgaa 2244
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APPLICANT: State//Frovince:
APPLICANT: Postal code/Zip: 32611
APPLICANT: Postal code/Zip: 32611
APPLICANT: Phone number: 904-392-6600
APPLICANT: Fax number: 904-392-6600
APPLICANT: Telex number: 904-392-6600
TITLE OF INVENTION: Cloning of Non-Iga FC Binding Forms of TITLE OF INVENTION: the Group B Streptococcal Beta Antigens CORRESPONDENCE ADDRESS:
ADDRESSEE: Sallwanchik & Saliwanchik STREFT: 2421 N.W. 41st Street, Suite A-1
CITY: Gannesville
STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3730;
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
2.9%; Score 68.8; DB 1;
Best Local Similarity 60.9%; Pred. No. 2.1e-08;
Matches 112; Conservative 0; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06111
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 Grinter Hall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Florida
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/242,932
FILING DATE: 16-MAX-1994
ATTORNEY_AGENT INFORMATION:
                                                                                                   NAME: SALIMANCHIK, DAVIG R. REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF142
TELECOMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application PC/TUS9506111 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Street address:
City: Gainesville
State/Province:
                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 3730 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: DNA (genomic)
US-08-714-481-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                linear
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PCT-US95-06111-8
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1757 ggacagcaacttattcatattatgctgtccccgttgccggaaaagatgaccaagtattag 1816
                                                        3024 TGACATTCACTTACTCTCACTTCGCAGTGCCGCAAGCC---AAAGGCAACAATGTGGTTA 3080
                                                                                                                                                                      caccgagtttcttactacaaattaacccggataacacaactactgtttagctaaaatga 1936
                                                                                                                                                                                                                                          1937 ctaatcaaggggattggatttgggatgattcaagcgaaaatcttgatatgattggtgatt 1996
                                                                                                                      3135 GCCCAAGCTTCTTAATCAACATCAAAGCCAATAAAACATCCGTTGTCAAAAACAGCATCC 3194
                                                                                                                                                                                                                                                                               3195 TGGAGCAAGGACAGCTGACAGTCAACTAATAACAGCAAAAAGAAAATGCCGATACTTCAT 3254
                                                                                             1817 ttacttcatatatgactaatagaaatggagtagcgggtaaaggaatggattcaacttggg
                                                                                                                                                                                                                                                                                                                                             3255 TGGCATTICITITATITCICAACAAGAIGGIGAA 3289
                                                                                                                                                                                                                                                                                                                  1997 tagactccgctgctttacctggcgaacgtgataaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 7, Application US/08923992A; Patent No. 6280738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARATERISTICS: LENGTH: 3294 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
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; LOCATION:
US-08-923-992A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2397 ATGTGTCAAAATCTGATGACACACTCAAAATCAACGGAGTGGAAGATCACAAAACGATTT 2456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1163 ttgaaggtgatggctattactaccaaacttatgatcaatgga-----aagctactaaca 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2457 ITGACGGAGACGGAAAAACATATCAGAACGTTCAGCAGTTATCGATGAAGGCAATTATA 2516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9gtaccttgtttttgaagcaagtactggtttggaaattatcaaggcgaggaccaaatt 1336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1337 ataactggttaaattatggcggagatgacgcatttaatatcaagagcttatttagaattc 1396
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                                                                                                                                                                                                                                                                                                                                  Length 3305;
                                                                                                                                                                                                                                                                                                                        Score 67.4; DB 3; Length 3
Pred. No. 4.5e-08;
0; Mismatches 506; Indels
NAME: FELTHAM, S. NEIL
REGISTRATION NUMBER: 36,506
REFERENCE/DOCKET NUMBER: CR-9807
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-92-6460
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3305 base pairs
TYPE: nucleic acid
STRANDENNES: single
                                                                                                                                                                                                                                   DNA (genomic)
                                                                                                                                                                                                                                                                                                                      Query Match 2.8%;
Best Local Similarity 46.9%;
Matches 495; Conservative
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; HYPOTHETICAL: NO
US-09-068-043-1
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ö GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Wilan S.
TITLE OF INVENTION: No. 6280738-19A FC Binding Forms of the Group B TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. Gaps ö Length 3294; Indels SOFTWARE: Patentin release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/923,992A FILING DATE: 05-SEP-1997 CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/024,707 FILING DATE: 06-SEP-1996 ATTORNEY/AGENT INFORMATION: ADDRESSEE: Sterne, Kessler, Goldstein & Fox P. STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Washington Score 64.2; DB 4; Pred. No. 3.1e-07; 0; Mismatches 113; 1438.0140001/RWE ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS 2.7%; Best Local Similarity 53.9 Matches 132; Conservative

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Conservative

Matches 132;

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2072 atgatectgetacaceaaatgatectgaaaegecaaetaeaecagaaaeeectgagaeae 2131
2012 tacctggcgaacgtgataaacctgttgattgggacttaattggttatggattaaaaccgc 2071
                       2132 ctaatacteccaaaacaccaaagactectgaaaateetgggaeaceteaaaetectaata 2191
                                                                                                                                                                     2192 cacetaatactccggaaattcctttaactccagaaacgcctaagcaacctgaaacccaaa 2251
                                                                                                                                                                                                                                                 2582 CACCGCATGTTCCGGAATCACCAAAGACTCCAGAAGGACCCAAAAGATTCCGGAACCCCCTA 2641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA FC Binding Forms of the Group B
TITLE OF INVENTION: Streptococcal Beta Antigens
CORRESPONDENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,992A
FILING DATE: 05-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1438.0140001/RWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08923992A
Patent No. 6280738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 14:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3312 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: 1...3
US-08-923-992A-3
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COUNTRY:
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2420 TACCTCAAGCCCCAGATACACCGCAGGCTCCAGACACGCCGTGTTCCGGAATCACCAA 2479
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                                                                                                                      2132 ctaatactcccaaaacacccaaagactcctgaaaatcctgggacacctcaaactcctaata 2191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: Streptococcal Beta Antigens
TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Ressler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                            2540 CGGAATCACCAAAAGGCCCCAGAAACACCGCGTGTTCCGGAATCACCAAAACACTCCAGAAG
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   Indels
0; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FLLING DATE: 05-SEP-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 05-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESENONA, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
MINIMALIANONINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08923992A Patent No. 6280738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202) 371-2600 TELEFAX: (202) 371-2540 INFORMATION FOR SEO ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3384 base pairs
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ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: CDNA
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US-08-923-992A-5
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Length 3384;

DB 4;

Score 64.2;

2.78;

Query Match

Score 64.2; DB 4; Length 3312; Pred. No. 3.1e-07;

2.78; 53.98;

Query Match Best Local Similarity

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                                                           tacctggcgaacgtgataaacctgttgattgggacttaattggttatggattaaaaccgc 2071
                                                                                                                                                      2465 AGGCCCCAGAAGCACCGCGTGTTCCGGAATCACCAAAGACTCCAGAAGCACCGCATGTTC 2524
                                                                                2072 atgatectgetacaceaaatgatectgaaacgeeaactaeaceagaaaeeectgagaeae 2131
                                                                                                                                                                                                                                 2525 CGGAATCACCAAAGGCCCCAGAAGCACCGCGTGTTCCGGAATCACCAAAGACTCCAGAAG 2584
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                                       Gaps
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Patent No. 6280738
GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Tai, Joseph Y.
TITLE OF INVENTION: No. 6280738-19A Fc Binding Forms of the Group TITLE OF INVENTION: Streptococcal Beta Antigens
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                         2132 ctaatacteccaaaacaccaaagactectgaaaateetgggacaceteaaacteetaata
       Pred. No. 3.1e-07;
0; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/923,992A
FILING DATE: 05-SEP 1997
CLASSIFICATION DATA:

APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP 1996
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
TELECOMMUNICATION:
       53.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202) 371-2600
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Best Local Similarity 53.9
Matches 132; Conservative
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STRANDEDNESS: single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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; LOCATION:
US-08-923-992A-9
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                                                                        2012 tacctggcgaacgtgataaacctgttgattgggacttaattggttatggattaaaaccgc 2071
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                                                    Gaps
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APPLICANT: Brady, L. Jeannine
TITLE OF INVENTION: Cloning of No. 5595740-IgA FC Binding Forms of
TITLE OF INVENTION: the Group B Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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            Length 3492;
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                                                  Indels
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      Score 64.2; DB 4;
Pred. No. 3.1e-07;
); Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SORTWARE: Patentin DATA:
APPLICATION NUMBER: US/08/242,932
FILING DATE: 16-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08242932
Patent No. 5595740
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NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 1775
TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100
Query Match 2.7%;
Best Local Similarity 53.9%;
Matches 132; Conservative (
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US-08-242-932-1
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2832 TACCTCAAGCCCCAGATACACCGCAGGCTCCAGACACACCGCATGTTCCGGAATCACCAA 2891

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2132 ctaatactcccaaaacaccaaagactcctgaaaatcctgggacacctcaaactcctaata 2191
2892 AGGCCCCAGAAGCACCGCGTGTTCCGGAATCACCAAAAGACTCCAGAAAGCACGCATGTTC 2951
                                                                                                                                                                                                                                                  3012 CACCGCATGTTCCGGAATCACCAAAAGACTCCAGAAGCACCAAAAGATTCCGGAACCCCTA 3071
                                                                                                                                       2952 CGGAATCACCAAAGGCCCCAGAAGCACCGCGTGTTCCGGAATCACCAAAGACTCCAGAAG
                                                                                                                                                                                                      2192 cacctaatactccggaaattcctttaactccagaaacgcctaagcaacctgaaacccaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Cloning of Non-IgA FC Binding Forms of TITLE OF INVENTION: Cloning of Non-IgA FC Binding Forms of TITLE OF INVENTION: the Group B Streptococcal Beta Antigens NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 Grinter Hall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Country:
Postal code/Zip: 32611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Phone number: 904-392-690
APPLICANT: Fax number: 904-392-6600
APPLICANT: Telex number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DALL.
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/242,932
APPLICATION NUMBER: US 08/242,932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application PC/TUS95061111 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Street address:
City: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICALE TO THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE TATE OF THE T
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PCT-US95-06111-1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 53.93
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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EDNESS: single
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PCT-US95-06111-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Brady, L. Jeannine
APPLICANT: Brady, L. Jeannine
TITLE OF INVENTION: Cloning of No. 5766606-IgA Fc Binding Forms of
TITLE OF INVENTION: the Group B Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                      2072 atgatectgetacaeccaaatgatectgaaaegecaaetaeaeccagaaaeceetgagaeae
                                                                                                                                 2132 ctaatactcccaaaaccacaaagactcctgaaaatcctgggacacctcaaactcctaata
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53.9%; Pred. No. 3.4e-07;
iive 0; Mismatches 113; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,481
FILING DATE: 16-SEP-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
FILING DATE: 16-SEP-1996
FILING DATE: 16-SEP-1996
ATTORNEY APPLICATION NUMBER: US 08/242,932
FILING DATE: 16-MAY-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF142
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-008-714-481-1
Sequence 1, Application US/08714481
Patent No. 5766606
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4200 base pairs
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Best Local Similarity 53.99
Matches 132; Conservative
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MEDIUM TYPE: Floppy
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COUNTRY: US
ZIP: 32606
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ö Indels 113; 2.7%; Score 64.2; DB 5; 53.9%; Pred. No. 3.4e-07; Live 0; Mismatches 113;

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us-09-995-587a-2.rni

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TYPE: NUCLEIC ACID
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US-07-638-431-1
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2832 TACCTCAAGCCCCAGATACACCGCAGGCTCCAGACACACGCATGTTCCGGAATCACCAA 2891
                                              2192 cacctaatactccggaaattcctttaactccagaaacgcctaagcaacctgaaacccaaa 2251
                                                                                                                                                                                                3012 CACCGCATGTTCCGGAATCACCAAAGACTCCAGAAGCACCAAAGATCTCCGGAACCCCTA 3071
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT. Tal, Joseph Y.
APPLICANT. Tal, Joseph Y.
APPLICANT. Tal, Joseph Y.
TITLE OF INVENTION: No. 6280738-IgA FC Binding Forms of the Group B TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Mashington
STATE: D.C.
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Best Local Similarity 53.9%; Pred. No. 4.3e-07;
Matches 131; Conservative 0; Mismatches 112; Indels
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COMPUTER: IBM PC compatible
OPERATE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/923,992A
FILING DATE: 05-SEP-1997
CLASSIFICATION: 536
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SPE-1996
ATTOKNEY AGENT INFORMATION:
REGISTATION NUMBER: 1438.014000
REEFERNCE/DOCKET NUMBER: 1438.014000
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
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SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
TYPE: NUCLEIC SIGIL
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Patent No. 6280738
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
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US-08-923-992A-1
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Search completed: September 22, 2002, 05:22:06 Job time: 20661 sec us-09-995-587a-2.rng

Page 1

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2. (SIDSI)/gcgdata/geneseqn-embl/NA1981.DAT:*
3. (SIDSI)/gcgdata/geneseqn-embl/NA1981.DAT:*
4. (SIDSI)/gcgdata/geneseqn-embl/NA1981.DAT:*
5. (SIDSI)/gcgdata/geneseqn-embl/NA1981.DAT:*
5. (SIDSI)/gcgdata/geneseqn-embl/NA1981.DAT:*
6. (SIDSI)/gcgdata/geneseqn-embl/NA1985.DAT:*
7. (SIDSI)/gcgdata/geneseqn-embl/NA1986.DAT:*
8. (SIDSI)/gcgdata/geneseqn-embl/NA1980.DAT:*
9. (SIDSI)/gcgdata/geneseqn-embl/NA1980.DAT:*
10. (SIDSI)/gcgdata/geneseqn-embl/NA1980.DAT:*
11. (SIDSI)/gcgdata/geneseqn-embl/NA1980.DAT:*
12. (SIDSI)/gcgdata/geneseqn-embl/NA1991.DAT:*
13. (SIDSI)/gcgdata/geneseqn-embl/NA1992.DAT:*
14. (SIDSI)/gcgdata/geneseqn-embl/NA1992.DAT:*
15. (SIDSI)/gcgdata/geneseqn-embl/NA1992.DAT:*
16. (SIDSI)/gcgdata/geneseqn-embl/NA1992.DAT:*
17. (SIDSI)/gcgdata/geneseqn-embl/NA1993.DAT:*
18. (SIDSI)/gcgdata/geneseqn-embl/NA1999.DAT:*
19. (SIDSI)/gcgdata/geneseqn-embl/NA1999.DAT:*
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22. (SIDSI)/gcgdata/geneseqn-embl/NA2001.DAT:*
23. (SIDSI)/gcgdata/geneseqn-embl/NA2001.DAT:*
24. (SIDSI)/gcgdata/geneseqn-embl/NA2001.DAT:*
25. (SIDSI)/gcgdata/geneseqn-embl/NA2001.DAT:*
26. (SIDSI)/gcgdata/geneseqn-embl/NA2001.DAT:*
27. (SIDSI)/gcgdata/geneseqn-embl/NA2001.DAT:*
28. (SIDSI)/gcgdata/geneseqn-embl/NA2001.DAT:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1736436 seqs, 858457221 residues
                                                                                                                              OM nucleic . nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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2367
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Vector pdenbell se SacB and cpy chime SacB and cpy chime DNA encoding novel DNA encoding novel DNA encoding novel DNA encoding novel DNA encoding novel DNA encoding novel
SUMMARIES	ID	AA235988 AA257329 AA257330 AA85233 AAS77631 AAS865008 AAS86581 AAS86581 AAS86736 AAS91108
	DB	23 23 23 23
	Match Length DB	10317 1668 1722 2537 2787 2787 2787 2787 2787 2787 2787
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	Score	80 78.4 78.4 71.8 71.8 71.8 71.8
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Result		U

	c 110 c 112 c 13 14 15 16	70.270.270.270.29		2079 2079 2079 2079 2325 3084	2222222	AAS85786 AAS85998 AAS87342. AAS88703 AAS69777 AAS75941	DNA encoding no DNA encoding n	8666666
····		68.8 68.2 68.2 68.2 67.8 67.8	000000	3084 3730 2745 5912 1690 1690	23 23 23 23 23 23	AAS87383 AAT03195 AAS73811 AAS86048 AAS86019 AAS86019		100 100 100 100 100 100 100
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RES AAZ ID XX XX AC XX DT	82 2 1	1 5988 s 5988; EB-200	tandard;	DNA; entr	10317	G G		
XX XX XX XX XX OS	Vect DNA trun	pGe quen ted	ell ng v cz;	nence or; ne jin of	SEQ sted	ID NO:1. deletion; transpos; lication; pGenDell;	ltion; contig; mapping; ss.	
XX XX WO XX XX WO XX XX XX XX XX XX XX XX XX XX XX XX XX	21-0CT 09-APR	UCRELIC. 1953044-A2 OCT-1999. APR-1999; APR-1998;	· · · · ·	-IB006	90.			
X X Y X X X X X X X X X X X X X X X X X	ESS III		Tanaka Tanaka 3040/03	H; H; Actor:		used for sequencing large	ge regions of DNA	

present invention describes a vector a high copy number origin of restrate Claim 43; Page 93-96; 102pp; English

(a) a high copy number origin of replication (Ori) having at least one cloning site, with at least one cloning site being positioned in the high copy number ori such that the ability of the high copy number Ori to direct replication is not disrupted when no insert has been cloned into the cloning site and is disrupted when an insert is cloned into the cloning site and is disrupted when an insert is cloned into the cloning site; and (b) a low copy number ori. Also described is a truncated Lacz gene to disringuish cells with the truncated Lacz gene to disringuish cells with the truncated Lacz gene to disribute when grown on medium containing Xgal and IPTG. Products and methods from the present invention can be used for the manipulation of DNA. They can be used for sequencing large regions of DNA and mapping the locations of markers within large regions of NB. The present sequence represent a specifically claimed vector following: comprising the sequence from the present invention. 

Sequence 10317 BP; 2567 A; 2296 C; 2469 G; 2985 T; 0 other;

; 9 1043 caagggtagacacgtctgataacaataccaatcatcaaaaaaattgctagcgctactcttt 1102 C-----TGATTTCTCCGGTAAACATTACGGCAAACAACAACTGACAACTGCACAAGTTA 8209 ttgaaggtgatggctattactaccaaacttatgatcaatgga---aagctactaacaaag 1219 gigocgataatatigoaatgogigatgotoatgiaatigaagatggiaatggigatoggi 1279 cacaagaatggtcaggatcagctgttttgaacagtgataactctatccaattattttata 1042 TTGACGGTGACGGAAAAACGTATCAAAATGTACAGCAGTTCATCGATGAAGGCAACTACA 8089 accttgttttttgaagcaagtactggtttggaaaattatcaaggcgaggaccaaatttata 1339 7968 TTAACAAAGCATACTATGGCAAAAGCACATCATTCTTCCGTCAAGAAAGTCAAAAACTTC 7909 ccaatgatgatattaagagtcgggcaacttgggctaatgcagctatcggtatcctcaaac 1459 TAAACGATGATTACACACTGAAAAAGTGATGAA------ACCGCTGATTGCATCTA 7798 1520 caatggtaagcgatgaaattgagcgaccaaatgtagttaaattaggtaataatact 1579 ACACAGTAACAGATGAAATTGAACGCGCGAACGTCTTTAAAATGAACGGCAAATGGTATC 7738 TGTICACTGACTCCGGGGATCAAAATGACGATTGACGGCATTACGTCTAACGATATT 7678 Gaps atttaactgataataggaaatgtatcactcgctcaggtacgaaatgactatattgtat GCTCAGGCGACAACCATACGCTGAGATCCTCACTACGTAGAAGATAAAGGCCACAAAT actggttaaattatggcggagatgacgcatttaatatcaagagcttatttagaattcttt taaataaggacgaaaagaatcctaaggtggcagagttatactcaccattaatttctgcac tatttgccgctacccgtttaaatcgaggaagtaatgatgatgcttggatgaatgctaatt 48; Score 80; DB 21; Length 10317; Pred. No. 2.5e-08; ); Mismatches 460; Indels 48 ö 3.48; Matches 464; Conservative Local Similarity Query Match 8322 1103 983 8262 8148 8088 1280 8028 1340 1400 7848 7977 1580 1163 1220 1460 7737 õ g õ g g ò g a ö ò g ò 셤 ò ò 8 ð g 8 음

ataagccattaaatgattctggagtagtcttgactgcttctgttcctgcaaactggcgga 1759 Method for improving plant salt resistance using transgenic technology ACAAGCCGCTGAACAAAACTGGCCTTGTGTTAAAAATGGATCTTGATCCTAACGATGTAA cagcaacttattcatattatgctgtccccgttgccggaaaagatgaccaagtattagtta cttcatatatgactaatagaaatggagtagcgggtaaaggaatggattcaacttgggcac CAAGCTATATGACAAACAGAGGATTCTACGCAGACAAA-----CAATCAACGTTTGCGC cgagtttcttactacaaattaacccggataacacaactactgttttagctaaaatgacta Levansucrase; SacB; cpy; salt tolerance; vacuole guide pept carboxypeptidase A; chimeric gene; transgenic plant; yeast; Bacillus subtilis 168; Saccharomyces cerevislae X8; SCI. cerevisiae. ACAD AAZ57329 standard; DNA; 1668 BP Claim 6; Page 2; 12pp; Chinese. SacB and cpy chimeric gene #1. Chimeric · Saccharomyces ceres Chimeric · Bacillus subtills. (GENE-) INST GENETICS CHINESE 98CN-0101336. 98CN-0101336 (first entry) Zhang H, Dong W; drought resistance; ds. 7407 AACAAGGACAAT 7396 1940 atcaaggggatt 1951 WPI; 2000-087902/08. 08-APR-1998; 03-APR-2000 08-APR-1998; CN1231337-A. 13-0CT-1999 Chen S, 7638 1760 7578 1820 1880 1700 7521 AA257329 ò qq qq Qγ g ò g

Sequence 1668 BP; 578 A; 372 C; 325 G; 393 T; 0 other;

present invention.

7677 A-----

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atgccgttggtgataatgttgcaatggtcggatatgttgctgatagtctaactggatctt

A method has been developed for raising salt tolerance of plants using transgenic technology. The method comprises: cloning levansucrase gene SacB and vacuole guide peptide (cpy) sequence of carboxypeptidase A from Bacillus and DNA of yeast, using the two kinds of gene to create a chimeric gene, and using the chimeric gene to structure plant expression plant and screen for resistant seedlings. The method can obtain a drought-resistant salt-tolerance plants, and the polymerase chain reaction (PCR) and Northern analysis of transgent plants shows that the exogenous gene is integrated in the salt-tolerance transgenic plant. The present sequence represents a SacB and cpy chimeric gene from the

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                                               caagggtagacacgtctgataacaataccaatcatcaaaaaattgctagcgctactctt 1102
                                                                                                                                          atttaactgataataatggaaatgtatcactcgctcaggtacgaaatgactatattgtat 1162
                                                                                                                                                                                         ttgaaggtgatggctattactaccaaacttatgatcaatgga...aagctactaacaaag 1219
                                                                                                                                                                                                                                                               gctcaggcgacaaccatacgctgagagatcctcactacgtagaagataaaggccacaaat 1018
                                                                                                                                                                                                                                                                                                    actggttaaattatggcggagatgacgcatttaatatcaagagcttatttagaattcttt 1399
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     Length 1668;
                           Indels
   DB 21;
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 Score 78.4; DB 21
Pred. No. 3.6e-08;
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3.3%;
llarity 47.6%;
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A method has been developed for raising salt tolerance of plants using transgenic technology. The method comprises: cloning levansucrase gene SacB and vacuole guide peptide (cpy) sequence of carboxypeptidase A from Bacillus and DNA of yeast, using the two kinds of gene to create a chimeric gene, and using the chimeric gene to structure plant expression plant and screen for resistant seedlings. The method can obtain adrought-resistant salt-tolerance plants, and the polymerase chain reaction (PCN) and Northern analysis of transgenic plants shows that the exogenous gene is integrated in the salt-tolerance transgenic plant. The present sequence represents a SacB and cpy chimeric gene from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resistance using transgenic technology
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                                                                                                                                                        peptide;
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                                                                                                                                                Levansucrase; SacB; cpy; salt tolerance; vacuole guide pept
carboxypeptidase A; chimeric gene; transgenic plant; yeast;
Bacillus subtilis 168; Saccharomyces cerevisiae X8;
drought resistance; ds.
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Pred. No. 3.6e-08;
0; Mismatches 461;
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Chimeric - Bacillus subtilis.
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                            AAZ57330 standard; DNA; 1722
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                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) INST
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medical imaging; diagnostic; genetic disorder; ss.
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30-MAR-2001; 2001WO-US08631

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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase data also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in capposities, for generic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and canno acid sequences. AAS6419-AAS94564 represent novel human conditional partners are discussed and polynuclectide sequences of the invention.

Committee the sequences data for this partent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                       wew issuated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
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                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 18127; 103pp; English.
                                                                                                                              Tang YT;
                    31-MAR-2000; 2000US-0540217.23-AUG-2000; 2000US-0649167.
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                                                                                  HYSE-) HYSEQ INC
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The colynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations capponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed security in the activity in the activity of the contract of the product of the product of the product of the product of the printed of the contract of the product of the product of the printed of the contract of the product of the printed of the product of the printed of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the product of the prod
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Conditional and polynucleotide sequences of the invention.

Conditional activity of the invention.

Coding sequences of the invention.

Coding sequences of the invention.

Coding sequences of the invention.

Coding sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO contribution.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,

Claim 1; SEQ ID No 21812; 103pp; English.

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, and polymerase chain reaction (PCR) primers, oligomers, and for chromosome polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating at language of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
         ----catgcttggttatgtatcaaactctttaaccggcccttaca 1051
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food supplement; medical imaging; diagnostic; genetic disorder;
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The polypeptide and polynucleotide sequences have applications in responsible, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp. Wipo.int/pub/published_pct_sequences.
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                                                                                                                                                               Sequence 2787 BP; 935 A; 596 C; 607 G; 649 T; 0 other;
                                                                                                                                                                                                                     Score 71.8; DB 23;
Pred. No. 1.3e-06;
0; Mismatches 482;
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          gtttettactacaaattaacccggataacacaactactgttttagetaaaatgactaatc
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                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                   novel human diagnostic protein #24540.
                                                                                                                        BP.
                                                                                                                     AAS88736 standard; cDNA; 2787
                                                                                                                                                                                                                                                                                                                 Tang YT;
                                                             1943 aaggggattggatttgg 1959
                                                                             1283 aaggacagctgacatgg 1299
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                                                                                                                                                                                                                                                                        31-MAR-2000; 2000US-0540217.
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P-PSDB; ABG24549.
                                                                                                                                                                                                                                                                                                              Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome configurates enhanced reaction (PCR) primers, oligomers, and for chromosome configuration of (II). The mapping, and in recombinant production of (II). The christian generating expressed genes. (I) is useful in gene therapy techniques (I) constone normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving or constituting a polypeptide in tissue, as molecular weight markers and as imaging of sites expressing (II). (II) and its binding partners are useful in medical cisorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cresponsible for genetic disorders or other traits to assess biodiversity amon acid sequences. AASA4197-AAS4454 represent novel human conditioning sequences of the invention.

Conditioning the printed in electronic format directly from WIPO the first of this patent did not appear in the printed constitution of the constitution of Claim 1; SEQ ID No 24540; 103pp; English.

ftp.wipo.int/pub/published\_pct\_sequences.

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1043 caagggtagacacgtctgataacaataccaatcatcaaaaaattgctagcgctactctt 1102
                                                                                                                                                                                                                                              1103 atttaactgataataatggaaatgtatcactcgctcaggtacgaaatgactatattgtat 1162
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                                                                                            42;
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Sequence 2787 BP; 935 A; 596 C; 607 G; 649 T; 0 other;
                                                                                     0; Mismatches 482;
                                                         DB 23;
                                                                         1.3e-06;
                                                     Score 71.8;
Pred. No. 1.
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, collypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The and gene mapping expressed genes. (I) is useful in gene therapy techniques of for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and useful in are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in tesponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and annoatic annoatic annoatic firman plant in medical disorders. Assetting and to produce other types of fata and products dependent on DNA and annoatic annoatic annoatic firman firman part in the father of the present novel human plant and products dependent on DNA and the products dependent on DNA and the product of the product of the present of the present plant of the present on DNA and the present of the present of the present of the present of the present of the present on DNA and the present of the prese Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss. New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess DNA encoding novel human diagnostic protein #26912. diagnostic coding sequences of the invention. Claim 1; SEQ ID No 26912; 103pp; English. BP AAS91108 standard; cDNA; 2787 Tang YT; 31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167. 30-MAR-2001; 2001WO-US08631 (first entry) 2001-639362/73. Drmanac RT, Liu C, (HYSE-) HYSEQ INC. P-PSDB; ABG26921 WO200175067-A2 13-FEB-2002 Homo sapiens 31-MAR-2000; 11-OCT-2001. biodiversity AAS91108; AAS91108 

Sequence 2787 BP; 935 A; 596 C; 607.G; 649 T; 0 other; ftp.wipo.int/pub/published\_pct\_sequences

. 2 42; Score 71.8; DB 23; Pred. No. 1.3e-06; 0; Mismatches 482; 3.0%; 453; Conservative Similarity Query Match Best Local Si Matches 453; 983 365 ò Q

Length 2787;

(first entry)

13-FEB-2002

caagggtagacacgtctgataacaataccaatcatcaaaaaattgctagcgctactctt 1102 1103 atttaactgataataatggaaatgtatcactcgctcaggtacgaaatgactatattgtat 1162 ccgataatattgcaatgcgtgatgctcatgtaattgaagatggtaatggtgatcggtacc 1282 ttgtttttgaagcaagtactggtttggaaaattatcaaggcgaggaccaaatttataact 1342 1343 ggttaaattatggcggagatgacgcatttaatatcaagagcttatttagaattcttcca 1402 1403 atgatgatattaagagtcgggcaacttgggctaatgcagctatcggtatcctcaaactaa 1462 425 ctgactattccggtaaacattacggcaaacaaagcctgacaacagcgcaggtaaatgtgt 484 1463 ataaggacgaaaagaatcctaaggtggcagagttatactcaccattaatttctgcaccaa 1522 1583 ttgccgctacccgtttaaatcgaggaagtaatgatgatgcttggatgaatgctaattatg 1642 tcactgattcacgcggttcaaaaatgacgatcgatggtattaactcaaacgatattta-- 1010 ......catgcttggttatgtatcaaactcttaaccggccttaca 1051 1703 agccattaaatgattctggagtagtcttgactgcttctgttcctgcaaactggcggacag 1762 1052 agccgctgaacaaaacagggcttgtgctgcaaatgggtcttgatccaaacgatgtgacat 1111 caacttattcatattatgctgtcccgttgccggaaaagatgaccaagtattagttactt 1822 1169 gctacatgacaaacagaggcttcttcgaggataaa-----aaggcaacattgcgccaa 1222 1223 gcttcttaatgaacatcaaaggcaataaaacatccgttgtcaaaaacagcatcctggagc 1282 taaaatctgatgacacactcaaatcaacggagtggaagatcacaaagcgatttttgacg 1163 ttgaaggtgatggctattactaccaaacttatgatcaatggaaagctactaacaaaggtg 605 gcgacaaccatacgctgagagacctcactacgttgaaga---caaaggccataaatacc 842 ataatgattacacattgaaaaaagtaatgaag------cggctgatcacttcaaaca 893 cggtaactgatgaaatcgagcgcgcgaatgttttcaaaatgaacggcaaatggtacttgt catatatgactaatagaaatggagtagcgggtaaaggaatggattcaacttgggcaccga gtttettactacaaattaacceggataacacaactactgttttagctaaaatgactaatc AAS85786 standard; cDNA; 2079 BP. 1943 aaggggattggatttgg 1959 1283 aaggacagctgacatgg 1299 AAS85786; 1223 1523 782 1011 1763 1823 RESULT 10 1883 AAS85786
ID AAS8
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DT 13-F ò Db δý QQ ò g ò Db οy q οχ g ò g òγ a ô a q à ò QQ δ Ω á qq οy q ŏ

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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
     DNA encoding novel human diagnostic protein #21590.
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P-PSDB; ABG21599.
                                                                                                                                                Liu C,
                                                                                                                                (HYSE-) HYSEQ INC.
                                                            WO200175067-A2.
                                               Homo saptens.
                                                                                                        31-MAR-2000;
23-AUG-2000;
                                                                                                                                                Drmanac RT,
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, colypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags (or identifying expressed genes. (I) is useful in gene therapy techniques of correstore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as imaging of sites expressing (II). (I) and its binding partners are useful in medical disorders involving aberrant protein expression or biological activity. (The polypeptide and polynucleotide sequences have applications in cresponsible for genetic disorders or other traits to assess biodiversity and or produce other types of data and products dependent on DNA and diagnostic coding sequences. AAS64197-AAS94564 represent novel human cold sequences and to this patent did not appear in the printed coperation, but was obtained in electronic format directly from WIPO specification, but was obtained in electronicat ftp.wipo.int/pub/published\_pct\_sequences. Claim 1; SEQ ID No 21590; 103pp; English.

Sequence 2079 BP; 710 A; 433 C; 475 G; 461 T; 0 other;

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991 tggtcaggatcagctgttttgaacagtgataactctatccaattattttatacaagggta 1050
                                                                      817 ggacaagttgctaattggaatggctatcaacttgtcatcgcaatggtgggaattccaaac 876
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                                              60;
 Score 70.2; DB 23; Length 2079;
Pred. No. 2.7e-06;
0; Mismatches 553; Indels 60;
   3.0%;
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                           Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
                          encoding novel human diagnostic protein #21802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 21802; 103pp; English.
                                                                                                                                                                                     Tang YT;
                                                                                                                     30-MAR-2001; 2001WO-US08631.
                                                                                                                                       31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
        13-FEB-2002 (first entry)
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Best Local Similarity 46.99
Matches 542; Conservative
                                                                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                                                                                   WPI; 2001-639362/73
                                                                                                                                                                (HYSE-) HYSEQ INC.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (I or identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical magning of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in clasponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic coding sequences. Assetled? Assetled represent novel human codis sequences and to produce other types of the invention.

CNOTE: The sequence data for this patent did not appear in the printed sequences. The sequence of the invention of security from WIPO.
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46.9%; Pred. No. 2.7e-06;
Live 0; Mismatches 553; Indels
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AAS87342 standard; cDNA; 2079 BP.

RESULT 12

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                                                                              GACTATTCCGGTAAACATTACGGCAAACAAAGCCTGACAACAGCGCAGGTAAATGTGTCA 1540
                                                                                                                                   AAATCTGATGACACACTCAAAATCAACGGAGTGGAAGATCACAAAACGATTTTTGACGGA 1480
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Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2079 BP; 710 A; 433 C; 475 G; 461 T; 0 other;
                                            DNA encoding novel human diagnostic protein #23146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 23146; 103pp; English.
                                                                                                                                                                                                        Tang YT;
                                                                                                                                         30-MAR-2001; 2001WO-US08631.
                                                                                                                                                           2000US-0540217.
2000US-0649167.
                            (first entry)
                                                                                                                                                                                                                      2001-639362/73.
                                                                                                                                                                                                      Drmanac RT, Liu C,
                                                            Human; chromosome
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                                                                                                       WO200175067-A2.
                                                                                        Homo sapiens.
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23-AUG-2000;
                          13-FEB-2002
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                                                                                                                         11-OCT-2001
         AAS87342;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, configurates chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of or identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polyucleotide sequences have applications in capanostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity min, and to and to produce other types of data and product dependent on DNA and main, and the produce of the pr 8 amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO 937 tggaagaatgtaggtccaatttttggctataattctacc----gcggtttcacaagaa 990 ggacaagttgctaattggaatggctatcaacttgtcatcgcaatgatgggaattccaaac 876 caaaatgataatcatatctatcttatataaaagtatggtgataatgaattaagtcat 936 307 acgctgatgacacatcaatctacatgttttatcaaaagctggaaaaacgcgggccgtgtc 90; 3.0%; Score 70.2; DB 23; Length 2079; 46.9%; Pred. No. 2.7e-06; Live 0; Mismatches 553; Indels 60; Conservative Similarity Best Local Sim Matches 542; Query Match 817 247 877

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                                                                                                                                        481 gactattccggtaaacattacggcaaacaaggcctgacaacagcgcaggtaaatgtgtca
                                                                                                                                                                                                                                                                                                                            661 gacaaccatacgctgagagaccttcactacgttgaaga---caaaggccataaatacctt
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Sequence 2079 BP; 461 A; 475 C; 433 G; 710 T; 0 other;
                                    DNA encoding novel human diagnostic protein #24507.
                                                                                                                                                                                    Claim 1; SEQ ID No 24507; 103pp; English.
   AASS8703 standard; cDNA; 2079
                                                                                                                                   Tang YT;
                                                                                                       31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                            30-MAR-2001; 2001WO-US08631
                           (first entry)
                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                           WPI; 2001-639362/73.
                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                 P-PSDB; ABG24516
                                                                        WO200175067-A2.
                                                              Homo sapiens.
                          13-FEB-2002
                                                                                  11-0CT-2001
                                               Human;
AAS88703/c
                                                     food
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741 GGACAGCTGACATGG 727 1051 1171 1225 1285 1525 1131 1705 1765 1825 1945 912 855 801 qq ò g ò Op ò Q g ò δ qq δ Dp ò g Ω QQ ŏ Q. ò g óγ g ò qq ò q ò qq δ qq οý qq The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome polynucleotides are also used in diagnostics as expressed sequence tags (C for identifying expressed genes. (I) is useful in gene therapy techniques (C to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as inging of sites expressing (II) (I) are useful in medical activity of a food supplement. (II) and its binding partners are useful in medical c disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the produce other types of data and products dependent on DNA and to produce other types of data and products dependent on DNA and to produce other types of data and products dependent on DNA and cold sequences. AAS64197-AAS4564 represent novel human of diagnostic coding sequences of the invention.

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C diagnostic coding sequence and for this patent did not appear in the printed control that the pri 8 1773 ACGCTGATGACATCAATCTACATGTTTTATCAAAAGCTGGAAAAACGCGGGCCGTGTC 1714 ggacaagtigctaatiggaatggctatcaactigtcatcgcaatgatgggaattccaaac 876 caaaatgataatcatatctatcttatataaaagtatggtgataatgaattaagtcat 936 stromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder; ss. New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodiversity 90; DB 23; Length 2079; Indels 3.0%; Score 70.2; DB 23; 46.9%; Pred. No. 2.7e-06; tive 0; Mismatches 553; Conservative of Similarity 542; Conserv. Query Mato Best Local Matches 817 877

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tggtcaggatcagctgttttgaacagtgataactctatccaattattttatacaagggta 1050 1111 gataataatggaaatgtatcactcgctcaggtacgaaatgactatattgtatttgaaggt 1170 1713 TITAAAGACAGGGATAAGIICGACGCCAACGAICCGATCCTGAAAGATCAGACGAAGAA 1654 1539 AAATCTGATGACACACTCAAAATCAACGGAGTGGAAGATCACAAAACGATTTTTGACGGA 1480 1479 GACGGAAAAACATATCAGAACGTTCAGCAGTTAATCGATGAAGGCAATTATACATCCGGC 1420 tggaagaatgtaggtccaatttttggctataattctacc----gcggtttcacaagaa 990 1419 GACAACCATACGCTGAGAGACCCTCACTACGTTGAAGA----CAAAGGCCATAAATACCTT 1363 1362 GTATTCGAAGCCAACAGGGAACAGAAAACGGATACCAAGGCGAAGAATCTTTATTAAC 1303 gtttttgaagcaagtactggtttggaaattatcaaggcgaggaccaaatttataactgg 1344 1345 ttaaattatggcggagatgacgcatttaatatcaagagcttatttagaattcttccaat 1404 1302 AAAGCGTACTACGGCGGCGCGCGCACGAACTTCTTCCGTAAAGAAGGCCAGAAGCTTCAGCAG 1243 1242 AGGCCTAAAAAAGGGGATGCTGAGTTAGGGAGGGGGCCCTGGGTATCATAGAGTTAAAT 1183 aaggacgaaaagaatcctaaggtggcagagttatactcaccattaatttctgcaccaatg 1524 1585 gccgctacccgtttaaatcgaggaagtaatgatgatgcttggatgaatgctaattatgcc 1644 1071 ACTGATTCACGCGGTTCAAAAATGACGATGGTATTAACTCAAACGATATTA---- 1014 1645 gttggtgataatgttgcaatggtcggatatgttgctgatagtctaactggatcttataag 1704 ccattaaatgattctggagtagtcttgactgcttctgttcctgcaaactggcggacagca 1764 tatatgactaatagaaatggagtagcgggtaaaggaatggattcaacttgggcaccgagt 1884 ttettaetaeaaattaaeeeggataacaeaetaetgttttagetaaaatgaetaatea 1944 1653 TGGTCCGGTTCTGCAACCTTTACATCTGACGGAAAATCCGTTTATTCTACAC----T gatggetattactaccaaacttatgatcaatgga-----aagetactaacaaaggtgcc gataatattgcaatgcgtgatgctcatgtaattgaagatggtaatggtgatcggtacctt 1405 gatgatattaagagtogggcaacttggggctaatgcagctatcggtatcctcaaactaaat 1182 AATGATTACACATTGAAAAAGTAATGAAG------CCGCTGATCACTTCAAACACG 972 CCGCTGAACAAAACAGGGCTTGTGCTGCAAATGGGTCTTGATCCAAACGATGTGACATTC acttattcatattatgctgtccccgttgccggaaaagatgaccaagtattagttacttca 9999attggatttgg 1959 937 991 ò g ò

atttaactgataataatggaaatgtatcactcgctcaggtacgaaatgactatattgtat 1162

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atgtgtcaaaatctgatgacacactcaaaatcaacggagtggaagatcacaaaacgatt

ttgaaggtgatggctattactaccaaacttatgatcaatgga----aagctactaaca 1216

629

1163

us-09-995-587a-2.rng

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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags (or identifying expressed genes. (I) is useful in gene therapy techniques (I) restore normal activity of (II) or to treat disease states involving (I) (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and its binding partners are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in capponsible for genetic disorders or other traits to assess biodiversity cand to produce other types of data and products dependent on DNA and diagnostic coding sequences. AAS64197-AAS94564 represent novel human cod diagnostic coding sequences of the invention.

CNOVE: The sequence data for this patent did not appear in the printed confined in electronic format directly from WIPO
                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2325 BP; 713 A; 593 C; 566 G; 453 T; 0 other;
                                                                                                                                              encoding novel human diagnostic protein #5581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 5581; 103pp; English.
                                   AAS69777 standard; cDNA; 2325 BP.
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2000US-0649167.
                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                       13-FEB-2002
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23-AUG-2000;
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                                                                       AAS69777;
RESULT 14
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                   4AS69777
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aaggigccgataatatigcaaigcgigaigcicaigtaatigaagaiggiaaiggigaic 1276
                                                                                                   ggtaccttgtttttgaagcaagtactggtttggaaaattatcaaggcgaggaccaaattt 1336
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                                                                                                                                                                                                                                                                                                           aactaaataaggacgaaaagaatcctaaggtggcagagttatactcaccattaatttctg 1516
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ttgacggagacggaaaaacatatcagaacgttcagcagtttatcgatgaaggcaattata 718
                                                               catcoggogacaaccatacgotgagagacoctcactacgttgaaga---caaaggocata 775
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2.9%; Score 69; DB 23; Length 2325; 47.7%; Pred. No. 5.3e-06; 0; Mismatches 460; Indels

Conservative

Local Similarity nes 469; Conserv

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1043 caagggtagacacgtctgataacaataccaatcatcaaaaaattgctagcgctacttt 1102 

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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, or polymerase chain reaction (FCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving cuantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical disorders involving aberrant protein expression or biological activity. C maging of sites expressing (II). (I) and (II) are useful for treating the polypeptide and polynuclectide sequences have applications in capponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and classing sequences of the invention.

C amino acid sequences AAS6419-AAS94564 represent novel human consequence data for this patent did not appear in the printed system of the invention.

C hote: The sequence data for this patent did not appear in the printed system of the printed county was obtained in electronic format directly from WIPO xxx
                  Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss
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23-AUG-2000; 2000US-0649167.
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P-PSDB; ABG11754.
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                                                                            Homo sapiens
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mutations

Sequence 2325 BP; 713 A; 593 C; 566 G; 453 T; 0 other;

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                                                        983 cacaagaatggtcaggatcagctgttttgaacagtgataactctatccaattattttata 1042
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                                       54;
          Length 2325;
                    Pred. No. 5.3e-06;
0; Mismatches 460; Indels
       Score 69; DB 23;
 2.98;
              Local Similarity 47.7 res 469; Conservative
Query Match
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Search completed: September 22, 2002, 09:38:17 Job time: 27991 sec

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Database

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AF047518 CLODING V
AF004910 CLODING V
U17500 CLODING V
AF047519 CLODING V
AF048702 Site-spec
AC020857 Wuss muscu
AF397467 Ictalurus
AC044842 Homo sapi
AJ271723 Fugu rubr
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AV016024 Takifugu
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AF413051 Zea mays
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Lactobacillus.
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Hijum,S.A.
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Score

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961	99ctataattottaccgcggtttcacaagaatggtcaggatcagctgttttgaacagtgat 	Qy Db	2041 tgggacttaattg 
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Qy	1141	ggtgatggctattactaccaaacttatgatc	ō
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ΟY	1201	gtgccgataatattgcaatgcgtgatgctacatgtaattgaa	Ö
QQ	1201	GGAAAGCTACTAACAAAGGTGCCGATAATATTGCAATGCGTGATGCTCATGTAATTGAA	26
ΟŸ	1261	ggtaccttgttttgaagcaagtactggtttggaaaattatcaa	3
Dρ	1261	ATGGTAATGGTGATCGGTACCTTGTTTTTGAAGCAAGTACTGGTTTGGAAAATTATCAA	1320
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Οy	1441	tatcctcaaactaaataaggacgaaaagaatcctaaggtggcagagttatac	0
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qq	1801	ATGACCAAGTATTAGTTACTTCATATATGACTAATAGAAATGGAGTAGCGGGTAAAGGA	œ
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qa '	1861	GATTCAACTTGGGCACCGAGTTTCTTACTACAAATTAACCCGGATAACACAACTACT	σ
οy	1921	ttttagctaaaatgactaatcaaggggattggatttgggatgattcaagcgaaaatct	σ
qa	1921	TTTAGCTAAAATGACTAATCAAGGGGATTGGATTTGGGATGATTCAAGCGAAAATCTT	1980
ΟŸ	1981	Lagactccgctgctttacctggcgaacgtgataaacctgttgat	2040
QO	1981	ratgattggtgatttagactccgctgctttacc	040
Οy	2041	tgetacaccaaatgateetga	10
qα	2041	GGGACTTAATTGGTTATGGATTAAAACCGCATGATCCTGCTACAAA	100

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2160 Qy 361 aatacagccaae	2220 Db 388	2280 Qy 481	2340 Db 508	2340 51	601	661	-DEC-2001 Db	Qy 721 aaaaatatgcct	Db 748 AAAATATGCCT	Oy 781 gtatggattca 	841	Db 868 TATCAACTTGTC	Oy 901 ttatataataag	Db 928 TrararaaraaG	Oy 961 ggctataattct	Oy 1021 aactctatccaa	Gaps 0; Db 1048 AACTCTATCCAA	60	87 DD 1108	120	1300 QY 1201	20.	240   251 gatggtaatggt	267	300 1348 GGCGAGGACCAA 327 1348 GGCGAGGACCAA	
acgecaactacaccagaaaccettgagacactaatacteccaaaacaccaaagactect 		ccagaacgcctaagcaacctgaaacccaaactaataatcgtttgccacaactgaaat 	aatgccaataaagccatgattggcctaggtatgggaacattgcttagtatgtttggtctt		gcagaattaacaaacgtcgatttaac 2367 . 			Ax316615 Ax316615.1 GI:17899729		_	1 (sites) van Geel-Schutten, G. H., Rahaoui, H., Dijkhuizen, L. and van H. H., C. A.	Novel fructosyltransferases Patent: WO 0190319-A 3 29-NOV-2001,	TNO (NL) Location/Qualifiers	ce 1, .2394 /organism="Lactobacillus reuteri"	/db_xref="taxon:1598" 829 a 437 c 464 g 664	tch 100.0%; Score 2367; DB 6; Length 2394;	0; Indels 0;	atgtataaaagcggtaaaaattgggcagtcgttacactctcgactgctgggctggtattt	ATGTATAAAAAGCGGTAAAAATTGGGCAGTCGTTACACTCTCGACTGCTGCGCTGCTATTT	ggtgcaacaactgtaaatgcatccgcggacacaaatattgaaaacaatgattcttctact 	qtacaaqttacaacaqqtqataatattqctqttaaaaqtqtqaacacttqqaaaqtq		caagttagtgcagctagtgatacgactattagaacttctgctaatgcaaatagtgcttct	CAAGTTAGTGCAGCTAGTGGTACGACTATTAGAACTTCTGCTAATGCAAATAGTGCTTC	tctgccgctaatacacaaaattctaacagtcaagtagcaagttctgctgcaataacatca 	tctacaagttccgcagcttcattaaataacacagatagtaagaaggctcaagaaagtact
Qy 2101 Db 2101		Uy 2221 Db 2221			Qy 2341 Db 2341	RESULT	AX316615 LOCUS DEFINITION	ACCESSION VERSION	KEYWORD. SOURCE	ORGANISM	KEFERENCE AUTHORS	TITLE JOURNAL	FEATURES	sonr	BASE COUNT ORIGIN	Query	Best 1 Matche	Οÿ	Db 28	Oy 61 Db 88	Т		Qy 181	Dp 208	Oy 241 Db 268	

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1527 ORGANI	REFERENCE LGLagttaaa 1560 AUTHORS	1620 JOUR 1647 FEBATUR	1680 misc	17	18	99gtaaagga 1860 Query Match 	Qy 1 atgt.	7			AAGACTCCT 2187  Qy 241 tctgc	22		2 2		Qy 541 gcggg           Db 608 GCGCG	PAT 14-DEC-2001 Qy 601	
	1 tcaccattaatttctgcaccaatggtaagcgatgaaattgagcgaccaaatgtagttaaa 		5-0								acgccaactacaccagaaacccctgagacacctaatactcccaaaacaccaaagactcct				gcagaaattaacaaacgtcgatttaac 2367 		AX316616 Sequence 4 from AX316616	
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an Geel-Schutten, G.H., Rahaoui, H., Dijkhuizen, L. and van
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STRFTF
S.mutans fructosyltransferase gene, complete cds.
M18954
M18954.1 GI:153635
fructosyltransferase.
Streptococcus mutans (strain GS5) (clone: pSS22 and pTS102.) DNA.
Streptococcus mutans
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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Sireptococcus.

(bases 1 to 4305)

Shiroza,T. and Kuramitsu,H.K.
Sequence analysis of the Streptococcus mutans fructosyltransferase
gene and flanking regions
J. Bacteriol. 170 (2), 810-816 (1988)
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88115184
Draft entry and printed copy of sequence for [1] kindly provided H.K.Kuramitsv, 06-MAR-1988.
Location/Qualifiers
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Best Local Similarity
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Lactobacillus reuteri
Bacteria: Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
Lactobacillus.
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van Geel-Schutten,G.H., Rahaoul,H., Dijkhuizen,L. and
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Patent: WO 0190319-A 10 29-NOV-2001;
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WO0190319.
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KEYWORDS SOURCE ORGANISM

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Pred. No. 6.7e-109;
0; Mismatches 821;
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Best Local Similarity 59.0%;
Matches 1266; Conservative
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Streptococcus.

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Stathsam,C., Giffard,P.M. and Jacques,N.A.

The cell-bound fructosyltransferase of Streptococcus salivarius: the carboxyl terminus specifies attachment in a Streptococcus pordonii model system

AL J. Bacteriol. 175 (14), 4520-4527 (1993)

NE 932232

CE 2 (bases 1 to 3600)

Streptococcus

NE 30 acques,N.A.

Direct Submission

AL Submission

AL Cocation/Qualifiers

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/Ar vrof="fatoroccus salivarius"

/Ar vrof="fatoroccus salivarius"
                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus salivarius fructosyltransferase (ftf) gene, complete cds; uracil phosphoribosyltransferase gene, 5' end; IS1161 transsposase gene, 3' end.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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VLYTVKDGKDKKARDKPETPYSPTEGNHSVDDKTNRPGTSRPADNNQPSADKEDKPTN
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MYGTYNGYGOGTSLLNKAFYGRSOSFFKTEKDOLLIDTNKKHDASLANGALGIIELN
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YSDHHSSFARSFLLNIKGTKTSVISNSILQOGQLTIDNY
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TGDFFTNNIGIVECPDIFMMQSNDGNYKWILGTSANGKVSGEDNTYAYWYGNYGFKF
IADISTPKWLDYGFDWYAAVTFESENGSKNLKKRYALAWMNNWDYANNTPTIONRFNG
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GVCIPKYTNENGDIMSGSFVYDAQNTAGFGKGAIVAIVTQPSASMDKQEOFLWYSTDR
                                                                                                                                                                                                                                                                                        /translation="MNKLKIVKCILIGSMICSGIITQQTFASTNDMNYKETYGVSHIT
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DTDINWYDAKNVGIRLRESLDKKRHIDVGIFTEGKYSYVNRAYTGNPDKSKKYVESRA
PFDINNKKVHLRIFVDKVSVEVFIDDGKITYSNEVFPRPEDKGITLFSIKGKAVFKNI
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NKRHDVAGISYFCSTDGENMVYKGLAYNVEDALGSROWAGSAILDENGMVQFFYTATG
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SFRDPYFFEDPKTKKDYLIFEGNKGGKIEKMKPENIGDKLFRKNHIAPRGVENFNGNV
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YDGLYGFCGNSLRSNYKPLNGNGLYITNPTNDPYQTYSWYLVSGHDVLSFINEYHFNG
QLRYGGTFGPTLOISLKGYKSKIIGRLGEGVVTPAH"
6560. 8305.
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FDTNDPNNASTHRSOYCGLNYKYAEKARLNTTAGODYYLVIYSPSLIODTPILNDEIH
LTVGDPVLIYDSTTAVADNYITGPTGYSSIANINVTNVPTTAAVKDIYVRSLNDVAR
VSDFNYWKVMAPGESFWRDSGQOCNIGIDVNYVENGTNNVQLMGTWRFVFQAGVDPIS
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GNSVASAAGDKSNNAPVAKLDPYILNPESLKNGEITTNTOIAMIWSDTDADGDALSRA
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DKKWYYINKPSSNAGICNYTITITPTVLSSNSTYNSYRLMIGNKNDVEAMLSGIQNTI
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                                                                                                                                                                                                                        /protein_id="AAK79737.1"
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/gene="CAC1774"
/note="sacB2"
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Clostridium acetobutylicum ATCC824 section 174 of 356 of the
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Childress, D., Zeng, Q. and Smith, D.R.
Direct Submission
Submitted (24-JUL-2001) GTC Sequencing Center Production,
Finishing, and Bioinformatics teams, Genome Therapeutics Corp., 100
Beaver Street, Maltham, MA 02453-8443, USA
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GNYDSENNINNINFNKAMEQYKNKINNERRLEILEYKKELREWGIEFVNLVQASPK
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/db_xref="G1:1501-4761"
/db_xref=
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Nolling,J., Breton,G., Omelchenko,M.V., Markarova,K.S., Zeng,Q.,
Nolling,J., Breton,G., Omelchenko,M.V., Markarova,K.S., Zeng,Q.,
Labson,R., Lee,H.M., Dubois,J., Qiu,D., Hitti,J., Wolf,Y.I.,
Tatusov,R.L., Sabathe,F., Doucette-Stamm,L., Soucaille,P.,
Daly,M.J., Bennett,G.M., Koonin,E.V. and Smith,D.R.
Genome Sequence and Comparative Analysis of the Solvent-Producing
Bacterium Clostridium acetobutylicum
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Bacteria, Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
2341 GACTTTAAİGTAGATTATTATGCGGTATCGGGTTATGGTCTTAAACCACATACTTAİCCT 2400
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/organism="Clostridium acetobutylicum"
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/db_xref="taxon:1488"
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Clostridium acetobutylicum.
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801. .1544
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                                                                           /product="HAD superfamily hydrolase"
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IEGKDPNKALKILLIKRGDHPYMGCWAVPGGFVNINBGLSSACYRELKEETNVENVYF
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                                                                                                                                                                                                                                                                                                             GIDKIDTYNILLTSDDGETKIGYLYFEKFERNGVYTIKVPSYRLLEWSKEELAFDHIE
EIDCALERLKNKIEYTPIAFSRLPKYFTLREAQKVFEAILNLEKPLFRANFRKIKKM
VVETEKEKITSGRPATCYTFNEDWQHTFLDE"
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ALSSPRVGGIVDEIVRINBTLGRKKIFFLDEHTNNSTEFKSYAKHCLEGSLEAELI
PELKNEALLDSNTVMIPKNSVNGFHPAGFKKMLEBNESQIENYIICGCEVDICVSNFA
NTLKTYFNOKNMDKRTIIPSRAVEFEPFGTHDGDLMKIISLWEWQSNGIEIVDRVL"
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Pred. No. 1.3e-08;
0; Mismatches 572; Indels 105;
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//p.xref="G1:15024748"
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/transl_table=11
/product="Nudix (MutT-like) hydrolase"
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/gene="CAC1778"

/codon_start=1

/transl_table=11
ooy3. 9346
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8693. oaar
                                                      /codon_start=1
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9598. .10521
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/gene="CAC1777"
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/gene="CAC1776"
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                                                                      GCTAGTAATCAAGTTATAACAACTACTCAAGTGAATTTATCTCAACCAGATTCAAATACA
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HTG 17-JUL-2001

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     SEQUENCING
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El-Sayed, N. M., Ghedin, E., Song, J., Larkin, C., Wanless, D., Jones, K. Peterson, J., Hou, L., Zhao, H., Mason, T., Militscher, J., Pai, G., Van Aken, S., Utterback, T., Khalak, H.G., Gerard, C., Leech, V., Ullu, E., Melile, S., White, O., Adams, M.D., Donelson, J.E. and Fraser, C.M. Trypanosoma brucei GUTatlo.1 RPCI93-3H15 BAC genomic sequence
                                                                                                                                                                                                                                                                   2 (bases I to 155204)
B1-Sayed,N.M., Khalak,H. and Adams,M.D.
Direct Submitted (28-JUN-1999) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
Medical Center Dr, Rockville, MD 20850, USA
Modical Center Dr, Rockville, MD 20850, USA
** NOTE: This is a "working draft' sequence. It currently
** consists of I contigs. Gaps between the contigs
** are represented as runs of N. The order of the pieces
** The contigs of the pieces
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                                                                                                                                                                                                                                                                                                                                                                                                                 is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 155204: contig of 155204 bp in length.
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Pred. No. 3.5e-06;
0; Mismatches 385; Indels 0
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Trypanosoma brucei chromosome II clone IN PROGRESS ***, 1 ordered pieces. AC007926
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/chromosome="II"
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BCT 01-0CT-1996
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                                          508 ttaaaacaaggatgctgaaaacgttgtaaaaaaggcgggaattgatcctaacagtttaact
                                                                                       568 gatgaccagattaaagcattaaataagatgaacttctcgaaagctgcaaagtctggtaca
                                                                                                                                                                              628 caaatgacttataatgatttccaaaagattgctgatacgttaatcaaacaagatggtcgg
                                                                                                                                                                                                                                                                      688 tacacagttccattcttdaagcaagtgaaatcaaaatatgcctgccgctacaactaaa
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Fouet, A., Arnaud, M., Klier, A. and Rapoport, G.
Characterization of the precursor form of the exocellular
levansucrase from Bacillus subtilis
Biochem. Blophys. Res. Commun. 119 (2), 795-800 (1984)
84178454
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/note="put. rRNA binding site (URF)"
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/note="imp. inverted repeat A'"
446. .455
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/translation="MCKGQSVYFGVTPYIF"
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/note="pot. -10 region (sacB)"
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1. .2007
/organism="Bacillus subtilis"
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/db_xref="G1:40119"
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Bacillus subtilis
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/traislation="Mitkrpakoayu/Leptaallaggatgafaketnokpyketygis
Hitrhdmloipedoknekyovpefdsstiknissakgldymdswplonadgyvanyhg
Yhyrpalogdrianddysiywfygygetsidswrnagryfkdskedandsilkdoy
Gemsgafftsdgkirlytydsgkhygkgylttaqnnysadssliningyedyksif
DGGRYYONYOQFIDESUNSSDBHTLRDPHYVEDKGHKYLVFEANTGTEDGYGEES
LPNKAYYGKSTSFFROESQKLLQSDKRTABELANGALGMIELNDDYTLKKYWKPLIAS
NTYDEIERANYFKNNGKWYLFTDSRGSKMTIDGITSNDIYMLGYVSNSLTGPYKPLIN
KTGLYLKMDLDPNDYTFYSHRAYPQAKGNNYVITSYMTNRGFYADKGSTFAPSFLIN
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Pred. No. 3.3e-05;
0; Mismatches 460; Indels
binding site (sacB)"
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1916. 1928
/note-"inverted repeat B'"
1 422 c 370 g 495 t
                                                                                                                          _xref="SWISS-PROT:P05655"
                                           /codon_start=1
/transl_table=11
/product="levansucrase"
/protein_id="CAA26513.1"
/db_xref="G1:732568"
'note-"pot. rRNA
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3.4%;
Best Local Similarity 47.7%;
Matches 464; Conservative
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Cloning vector (pRL278) for sacB-mediated positive selection for L05083.1 G1.209132
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HITRHDMLOIPEQQKNEKYQVEEDSSTIKNISSAKGLEVWDSWPLQNADGTVANTHG
HITRHDMLOIPEQQKNEKYQVEEDSSTIKNISSAKGLEVWDSWPLQNANTHG
YHVFALAGDEKNADDTSIYMEYQKVGETSIDSWKNAGRVFKDSDKFDANDSILKDQT
QEWSGSAFTSDGKIRLYPTDESGKHYGKQTLTTAQNNYSABDSSLANINGVEDYKSIF
DGDGKTYQNVQQFIDEGNYSSGDNHTLRDPHYVEDKGHKYLVFEANTGTEDGYQGEES
LFNKAYYGKSTSFFRQESQKLLQSDKKRTAELANGALGANIELNDDYTLKKVWKPLIAS
NTYDELERANVFKMNGKWYLFTDSRGSKMTIDGITSNDIYMLGYVSNSLTGPYKPLN
KTGLVLKMDLDPNDVTFTYSTNDA
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Black, T.A., Cai,Y. and Wolk,C.P.
Spatial expression and autoregulation of hetR, a gene involved in
the control of heterocyst development in Anabaena
Unpublished (1992)
 tatttgccgctacccgtttaaatcgaggaagtaatgatgatgcttggatgatgctaatt 1639
                                                                1640 atgccgttggtgataatgttgcaatggtcggatatgttgctgatagtctaactggatct 1699
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                                                                                      CTTTACTTACTCACACTTCGCTGTACC---TCAAGCGAAAGGAAATGTCGTGATTA
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pattern formation in the
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/organism="unidentified cloning vector"
/db_xref="taxon:45196"
/note="sacB from B.subtills; ORF"
/codon_start=1
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/protein_id="AAA72307.1"
/db_xref="G1:209133"
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Cloning vector DNA.
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artificial sequence; vectors.
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Cai,Y.
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heterocyst differentiation and
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      /tranil_table=11
//protein_id=1a0="AAA/2308.1"
/db_xref="G1:2009.34"
/translation="MTEODGLHAGSPAAWVERLEGYDWAOQTIGCSDAAVERLSAGGR
YCTVATALSCALMELQDBARLSWILATGYPCAAVLDVYTEAGRDWLLLGEVPGQDL
ISSHIAPARKYSIMADAMRRIHILDPATGPFDHQAKIRIERRATRWEAGLYDQDDLDE
BHQGLAPABLERARKARMPDGEDLVYTHGDACLPNIHVENGRESGFIDGGRLGYADDRY
QDIALATRDIAELGGEWADRFLVYTGIAAPDSQRIAFYRLLDEFF"
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                                                                                                                                                                                                                                                                                                                                                              1163 tigaaggigatggctattactaccaaacttatgatcaatgga---aagctactaacaaag 1219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccaatgatgatattaagagtcgggcaacttgggctaatgcagctatcggtatcctcaaac 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           taaataaggacgaaaagaatcctaaggtggcagagttatactcaccattaatttctgcac 1519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tatttgccgctacccgtttaaatcgaggaagtaatgatgatgcttggatgaatgctaatt 1639
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                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1242 TTGACGGTGACGGAAAAACGTATCAAAATGTACAGCAGTTCATCGATGAAGGCAACTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                    gtgccgataatattgcaatgcgtgatgctcatgtaattgaagatggtaatggtgatcggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1182 GCTCAGGCGACAACCATACGCTGAGAGATCCTCACTACGTAGAAGATAAAGGCCACAAAT
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                                                                                            DB 12; Length 5941; 2.9e-05;
                                                                                                                                                                                                Score 80; DB 12; Length 594
Pred. No. 2.9e-05;
0; Mismatches 460; Indels
codon_start=1
                                                                                                                                                                                              3.48;
                                                                                                                                                                                                        Similarity 47.7
                                                                                                                                                 1419
                                                                                                   misc_feature
                                                                                                                         misc_feature
                                                                                                                                                                                                                     464;
                                                                                                                                                                                             Query Match
Best Local S
Matches 464
                                                                                                                                              BASE COUNT
ORIGIN
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SYNPRLA 6347 bp DNA circular SYN 27-APR-1993 Cloning vector (PRL271) for sacB-mediated positive selection for double recombinants in gram-negative bacteria.
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TLELVKRCNFVTAIEIDHKLCKTTENKLVDHDNFQVLAKDILGFKFPKNQSYKIYGNI
PYNISTDIIRKIVFDSIANEIYLIVEYGFAKRLLNTKRSLALLLMAEVDISILSMVPR
EYFHPKPKVNSSLIRLSRKKSRISHKOKQKYNYFVMKWVNKEYKKIFTKNQFNNSLKH
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cagcaacttattcatattatgctgtccccgttgccggaaaagatgaccaagtattagtta 1819
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                                                                                    672 CCTTTACTTACTCACTTCGCTGTACC---TCAAGCGAAAGGAAACAATGTCGTGATTA
                                                                                                                                                                                    1820 cttcatatatgactaatagaaatggagtagcgggtaaaggaatggattcaacttgggcac
                                                                                                                                                                                                                                                                         CAAGCTATATGACAAACAGAGATTCTACGCAGACAAA -----CAATCAACGTTTGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular genetic approaches towards the understanding of thererocyst differentiation and pattern formation in the cynobacterium Anabaena sp
Unpublished (1992)
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/note="erythromycin resistance determinant"
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Spatial expression and autorequiation of hetR, a (
the control of heterocyst development in Anabaena
Unpublished (1992)
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complement(473. .1894)
/note="sacB gene from B.subtilis; ORP"
/codon_start=1
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/protein_id="AAA72302.1"
/db_xref="G1:209126"
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/db_xref="GI:209127"
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unidentified cloning vector
artificial sequence; vectors
[1] (bases 1 to 6347)
cai,Y.
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3503. .4162 /note="chloramphenicol resistance determinant"

/codon\_start=1

AGIDDLNNISFEQFLSLFNSYKLFNK" 3503. .4162

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VERSION
KEYWORDS
SOURCE
ORGANISM
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SYNPRLB/c
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
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SSLMSEYHDDFRQFLHIYSQDVACYGENLAYFPKGFIENMFFVSANPWYSFTSPLNV
ANMDNFFAFVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
                                   translation="MEKKITGYTTVDISQWHRKEHFEAFQSVAQCTYNQTVQLDITAF"
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                                                                                                                                                                                                                                                                                   Caagggtagacacgtctgataacaataccaatcatcaaaaaattgctagcgctactcttt 1102
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                                                                                                                                                                                                                                                                                                                                                 C----TGATTTCTCCGGTAAACATTACGGCAAACAAACACTGACAACTGCACAAGTTA
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                                                                                                                                                                                                                                              48;
                                                                                                                                                  pMB1
                                                                                                                                                                                                                 Length 6347;
                                                                                                                                                                                                              Score 80; DB 12; Length 63
Pred. No. 2.8e-05;
); Mismatches 460; Indels
                                                                                                 4252. .5221
/note="multiple cloning sites"
5222. .6347
/note="oriv and oriT genes from Plasmid
1305 c 1404 g 1989 t
           /protein_id="AAA72304.1"
/db_xref="GI:209128"
/transl_table=11
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ilarity 47.7%;
Conservative
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                                                                                                     misc_feature
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Best Local S
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/ AB_ATRAFERE GET : 209130"
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/ LTAINS LA LIOO="MUNIKERROMTUTETSIDSWKRAGRVERDSWPLONANGTYANYGG
YHLYFALAGDPR MNADTSIYMFYOKVGETSIDSWKRAGRVERDSWPSANDSTLKDOT
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KTGLVLKMDLDDPNDYTETYSFRAVENTENTANTGYTSYMTNRGFYADKGSTFAPSFLLN
IKGKKTSVVKDSILEQGGLTVNK"
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KRELOGEGWORNDILAGIEPRATIDIDLAILLTRAREHSVALVGPAAEELFDPVPEO
DLFBALNETLETWORPDWAGDERNYVLTLSRIWYSAVTGKIAPKOVAADWAMERLPA
OYOPVILEARQAYLGOBEDRRASRADOLEBEYHYVKGEITKVVGK
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1 (bases 1 to 6798)

Cai, Y.

Molecular genetic approaches towards the understanding concepts differentiation and pattern formation in the Unpublished (1992)
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Black T.A., Cai.Y. and Wolk,C.P.
Spatial expression and autoregulation of hetR, a cthe control of heterocyst development in Anabaena Unpublished (1992)
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/db_xref="taxon:45196"
complement(473. 1894)
/note="sacB gene from B.subtilis; ORF"
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/db_xref="GI:209131"
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                                         Length 6798;
                                      Score 80; DB 12; Length 67;
Pred. No. 2.8e-05;
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                                                                                  linear
                                                                                  DNA
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Chumakov,I. and Tanaka,H.
High throughput DNA sequencing vector
Patent: US 6258571-A 1 10-JUL-2001;
Location/Qualifiers
1. 10317
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                                                                            Sequence 1 from patent US 6258571. ARI62197
                                                                                                                                                                                                                                                                  /organism="unknown"
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Best Local Similarity 47.79
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/db_xref="G1:1945642"
/db_xref="SPTEMBL:006965"
/translation="KYNYSYSYFGYVKSTEEDNLGVEYAFTLGCKNENOPCSLDEEKA
KNKVEKLINSITFLIDKKEK"
198. 2108
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DOLOI IS ESCSADNOSYNEFOLLGIDHSOVEATKRETUKAKKAGASONSDLKTFALG
HSLANNOVWOLIDGEYDEVYGVAGAQVNIDOLLETDESLYRVVIRKFSYKYEDIDS
IP PEKLKKETORYYEDKGVTTWITORLSKDDPLYGVSGKADFITFGDVKMADTWISVK
GIRNLEGOYPEDDVSTOKFLØXYKDDYSEKOLINGFIKAASGIDIDLIEKVKWIDGAL
KKVSVLEHFDDVYGWSTOKFLØXYKDDYSEKOLINGFIKAASGIDIDLIEKVKWIDGAL
KKVSVLEHFDDVYGWSTOKFLØXYKDOTENPORAN
IKKELTNINASWRGIESRYEHFIDHLKHGQFWQALKDVGEIVDVYKSILSSLKTLDTE
TKDALKLIVOGHSIVQMINALSKEKGFSYKGSDIYFTGKSGSCFTIQVULSSAVRIYO
NGMK IVEDMDEDAISKYGKVYSQEIDEDFIDKRQAITTAIHHMEENPSHYAFDLGFRLA
AGFSHTPDKLEKISVHESFHTGALPANDGIVAELKKOTTEKRDFIKNIRESIEKLFEK
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WLKSLYKTGEGDDYFFYWLSCSAYFRGHTDFAETTWRKVESGY PGEDRPAPWIERRE
ALPSSVEGRLAAYYISSTKGETEHLEAVIRSKRITAPPETHFYKLLLMODSAAADVSE
DALFAYGTVKLLGAEKEEMKTEVMSCWYFYIJQDIRAAAPEKNEKGWAAAICYIWKE
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DIRRIYKEETHHDLPENMKIEIYTSNELVNQNTSIQSSTRESGYDGTAIHIIDEKKHI
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QRAVHLEPEDSEMLSQLAVIYSEMGQYQESNDLLDYIMANLEAEMPECHYFKANNFAH
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2647. .4416
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Juent (88 kb).

Jue; CRH gene; levansucrase; para-nitrobenzyl
gene; pare; signa factor 54; ERNA-Arg gene;
yere gene; yvcB gene; yvcC gene; yvcB gene; yvcR gene; yvcB gene; yvcC gene; yvcB gene; yvcR gene; yvcB gene; yvcR gene; yvcB gene; yvcR gene; yvcR gene; yvcR gene; yvcH gene; yvdC gene; yvcR gene; yvcR gene; yvcH gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvdC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yvCC gene; yv
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Submitted (11-APR-1997) F.C. Denizot, C.N.R.S., Laboratoire De
Chimie Bacterienne, 31, Chemin J. Aiguier, Marseille Cedex 20,
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/codon_start=2
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Denizot, F.C.
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VDANDLIKGODGONGALLERRANGKARTSERAALAKKGEGEAAALIKKGEGEAAALIKKGEGEAAALIKKGEGEAAALIKKGEGEAAALIKKGEGEAAALIKKGEGEAAALIKKGEGEAAALIKKGEGEAAALIKKGEGEAAALIKKGEGEAAALIKKGEGEAAALIKKGEGEAAALIKKGEGEAAALIKGGGEAAKASGKGTGATTESSKASSSBDSSDNSSDNSSDNSSDNSSSNSSSRKSSSKKSSGRNSG
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GPVGGTTTDTLUGRGAVSASEMRRODLVFFDTYKTNGHVGITCGNGFFLNDNTSHGV
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                                    1880 cgagittcitactacaaattaacccggataacacaactactgitttagctaaaatgacta 1939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The complete genome sequence of the gram-positive bacterium Bacillus subtilis
Nature 390 (6657), 249-256 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
1 (bases 1 to 209510)
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complement(4. .29)
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299121.1 GI:2635827
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TITLE
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Db 136294

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGMDEETITHLFNRYYRGTNTKDSTAGTGLGLAIAKELVHLHNGTIHVNSRTNIGTVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note"similar to two-component sensor histidine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to RNA polymerase"
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                                                                                                                                                                                                                                                                                                                                                                                                                  function-"unknown"
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Db 136855 CAAGCTTCCTGCTGAACATCAAAGGCAACAAACATCTGTTGTTCTCAAAGACATCCTTG 136914

Qy 1940 atcaaggggatt 1951

Db 136915 AACAAGGACAAT 136926
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1700 ataagccattaaatgattctggagtagtcttgactgcttctgttcctgcaaactggcgga

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136644

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3.4%; Score 80; DB 1; Length 209510; llarity 47.7%; Pred. No. 1.9e-05; Conservative 0; Mismatches 460; Indels 48

Query Match Best Local Similarity

Matches 464;

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ALIGNMENTS

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ENKATYOLA, ENGALONDOMA.

ELENATOROMA.

Trypanosoma.

EL (bases 1 to 641)

RS El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C., Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J., Fraser,C. and Adams,M.

Determination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library

AL Unpublished (1999)

Contact: Najib M. El-Sayed

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Email: nelsayed@tigr.org

Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared

DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page: http://www.ligr.org/tdb/mdb/tbdb/.

Seq primer: M13-Reverse

Class: shotgun.

RESS

Location/Qualifiers

TRESS

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       AQ946120 641 bp DNA linear GSS 27-JAN-2000 Sheared DNA-46J23.TR Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-46J23, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Trypanosoma brucei
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                A0952743
CNS014J2
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AQ946120/c
LOCUS
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AUTHORS
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                                                              September 22, 2002, 01:51:26; Search time 7643.51 Seconds (without alignments).
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                                                                                                                              1 gttaacaaagacaaaatttt.....gttactgcttgcaaaagctt 4634
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     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ946120
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4634
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/organism="Trypanosoma brucei" /strain="REU927/4 GUTat 10.1" /db\_xref="taxon:5691" /clone="Sheared DNA-46733" /clone\_lib="Sheared DNA-4

source

AQ656218 AQ658275 AZ217550 CNS01JRG

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FEATURES

Wed

Best Local Matches

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BASE COUNT

ORIGIN

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/clone_lib-"Sheared DNA-42E2]"
/clone_lib-"Sheared DNA"
/clone_lib-"Sheared DNA"
/clone_lib-"Sheared DNA"
/note-"Vector: pUC18; Site_l: SmaI; Constructed at The
/nstitute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
sheared to give a tight size distribution (approx 2 kb).
                 El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.
betermination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                           Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: Ml3-Forward
Class: shotgun.
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                                                                                                                       Unpublished (1999)
Other GSSs: Sheared DNA-42E21.TR
Contact: Najib M. Bl.Sayed
Contact: Najib M. Bl.Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0200
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51.2%; Pred. No. 1.6e-07;
tive 0; Mismatches 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
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Best Local Similarity 51.2%
Matches 226; Conservative
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/note="Vector: pUC18; Site_1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma bruce! (TREU927/4 GUTAT 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + 1 method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun
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genomic clone
                                                                                                                                                                             sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
                                                                                                                                                                                                                                                                                                                                 Length 641;
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                                                                                                                                                                                                                                                                                                                                                                          275; Indels
                                                                                                                                                                                                                                                                                                                             Score 106; DB 12;
Pred. No. 4e-09;
0; Mismatches 275;
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Similarity 49.6%;
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8

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1630 atcagccgctactcaagcaaacttgaagaagctaaatcctcaagctgctaaggctgttca 1689
                               Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Eukaryottc Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Fax: 301 838 0208
Fax: 301 838 543
Email: 91oftuagetigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC Library was generated from A. gambiae EEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed saxes of larvae. The BAC
library was constructed at Texas A&W University BAC Center
                                                                                                                                                                                                                                             Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
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                                                                                                                       BH401326 687 bp DNA linear GSS 11-DEC-2001
AG-ND-155A14.TF ND-TAM Anopheles gambiae genomic clone AG-ND-155A14
, DNA sequence.
BH401336
                                                                                                                                                                                                                                                                                                   Anopheles.

1 (bases 1 to 687)
Shetty.J., Malek.J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J.
Direct Submission of BAC-end sequences from Anopheles gambiae
Unpublished (2001)
Other_GSSs: AG-ND-155A14.TR
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/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-155A14"
/clone=_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
/note="Vector: pECBAC1; Site_1: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.0%; Score 92.8; DB 12; Length 51.4%; Pred. No. 9.1e-07;
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1. .687
                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Brendan J Loftus
                                                                                                                                                                                                                                  African malaria mosquito.
attaatgaattaaataagatt 1750
                                                                                                                                                                                              BH401326.1 GI:17347542
                               680 AATAATAATAATAATAAT 700
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Seq primer: M13 For
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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/note="Genoscope sequence ID : COBGO95BD12LP1-end : T7"
/note="Genoscope sequence ID : COBGO95BD12LP1-end : T7"
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Roest-Crollus, H., Jaillon, O., Dasilva, C., Bouneau, L., Fish
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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/db_xref="taxon:99883"
/clone="095G24"
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43.9%; Pred. No. 1.6e-06;
tive 30; Mismatches 277;
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota: Meoptera: Endopterygota; Diptera; Nematocera; Culicoidea;
Sherty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J.
Direct Submission of BAC-end sequences from Anopheles gambiae
Other_GSSs: AG-ND-138G17.TF.1
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fex: 301 838 3543
Email: bjloftusétigr.org
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AG-ND-138G17 TR ND-TAM Anopheles gambiae genomic clone AG-ND-138G17
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       1500 gotgttgttaatgaaaacaaaaatactaacaatactgaaaatgctgttgttaatgaaaac 1567
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BH391984.1 GI:17338125
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Class: BAC ends.
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/organism="Anopheles gambiae"

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El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.
Determination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA, library
                                                                                                                                                                                                                                                                                                                                                          1374 ttggcgtagatggaaaaattattagtgctaacagtaatacaaccagtggctcgacaaatc 1433
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                      Length 832;
/db_xref="taxon:7165"
/clone="AG-ND-138617"
/clone=lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
71 c 59 g 277 t
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Other GSSs: Sheared DNA 49K6.TR
Contact: Najib M. Bl-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0208
                                                                                                                                                                               1.9%; Score 89.8; DB 12;
51.4%; Pred. No. 3.1e-06;
Live 0; Mismatches 217;
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Ürushihara,H.
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/strain="Trypanosoma bruce;"
/db_xref="taxon:5691"
/db_xref="taxon:5691"
/clone="sheared DNA"
/clone="sheared DNA"
/clone=lib="Sheared DNA"
/note="Vector: pUC18; Site_1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of Trypanosoma bruce; (TRE0927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotun sequencing projects. In Genome Sequencing: A Practical Appreach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU076358 AU07ctyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSA642, mRNA sequence.
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Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page: http://www.tigr.org/tdb/mdb/tbdb/. Seq primer: Mi3-Forward Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1359 aagctaatggtcaaattggcgtagatggaaaaattattagtgctaacagtaatacaacca 1418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtcaattaaagttaactaataatgaacaaccatcagccgctactcaagcaaacttgaaga 1658
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1 (bases 1 to 469)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.9%; Score 89.4; DB 12; Length 52.2%; Pred. No. 3.7e-06; tive 0; Mismatches 181; Indels
                                                                                                              Location/Qualifiers
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Matches 198; Conservative
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AU076358
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KEYWORDS
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AQ639568 401 bp DNA linear GSS 08-JUL-1999
927P1-4D3.TP 927P1 Trypanosoma brucei genomic clone 927P1-4D3, DNA
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1 (bases 1 to 401)
El-Sayed,N., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C., Garard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J., Fraser,C. and Adams,M.

Determination of clone end sequences from Trypanosoma brucei TREU
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                                                                                                                                                                                                                                               /strain="AX4"
/db_xref="taxon:44689"
/clone="SSA642"
/clone_lib="Dictyostellum discoideum SS (H.Urushihara)"
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Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
University of Tsukuba
Jaran Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA project in Japan.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 469;
                                                                                                                                                                                                                                                                                                                                                                 3 others
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                                                                                                                                                                                                                             /organism-"Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 84.6; DB 9;
Pred. No. 2.7e-05;
0; Mismatches 156;
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Unpublished (1999)
Other-GSSS: 927Pl-4DS.TV
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
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30 c 26
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AQ639568.1 GI:5116278
GSS.
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/clone_lib="Sheared DNA' 1302.
/clone_lib="Sheared DNA' 1302.
/clone_lib="Sheared DNA' 1302.
/clone_lib="Sheared DNA' 1302.
/note="Vector: pUC18; Site_l: Smal; Constructed at The Institute for Genomic Research (TIGR). Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the libraric construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999).
                                                                                               The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
721: 301 838 0200
722 Fax: 301 838 0208
723 Fax: 301 838 0208
724 Email: nelsayedtigr.org
725 Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
726 DNA library constructed at TIGR. Clones will be available for
727 distribution through ATCC. Sheared DNA end sequences search page:
728 primer: MJ3 Reverse
728 Closs: shotgun.
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AU086536 AU086536.1 GI:12388677
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53.9%; Pred. No. 0.00011;
tive 0; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
            Other_GSSs: Sheared DNA-43D2.TF
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="Sheared DNA-43D2"
                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Matches 10
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KEYWORDS
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            COMMENT
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                                                                                                                                                                                                                                                                                                                            /organism="Trypanosoma brucei"
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1 (bases 1 to 621)

El-Sayed,N., Zhao, H., Gill,S., Suh,E., Malek,J., Fujii,C., Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J., Fraser,C. and Adams,M.
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10.1 sheared DNA library
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ941683 621-bp DNA linear GSS 27-JAN-20
Sheared DNA-43D2.TR Sheared DNA Trypanosoma brucei genomic clone
Sheared DNA-43D2, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                   Email: nelsayed@tigr.org
For clone/filter availability, please contact Sara Melville
(sml60@mole.bio.cam.ac.uk). Pl end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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   Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 82.6; DB 12;
Pred. No. 6.1e-05;
0; Mismatches 129;
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                                                                                                                                                                                                                                                                         Location/Qualifiers
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AQ941683.1 GI:6764948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.8%;
Best Local Similarity 55.4%;
Matches 160; Conservative
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9712 Medical Cent.
Tel: 301 B38 0200
Fax: 301 B38 0208
                                                                                                                                                                                                                   Seq primer: SP6
Class: P1 ends.
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Gaps

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Length 621; Indels EST 27-JAN-2001

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Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
                                                                                                                                                                                     Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J. Direct Submission of BAC-end sequences from Anopheles gambiae Direct Submission of BAC-end sequences from Anopheles gambiae (Dupublished (2001) Other GSS: AG-ND-180F9. TR Contact: Brendan J. Loftus Department of Enkaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                Email: b)loftusetigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA.from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M Universty BAC Center
University. College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 81; DB 12; Length 77
Pred. No. 0.00012;
0; Mismatches 110; Indels
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/clone="AG-ND-180F9"
/clone=lib="ND-TAM"
/note="Vector: pBCBAC1; Site_1: HindIII"
125 c 99 g 240 t
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                                                                             African malaria mosquito
                                BH391959.1 GI:17338087
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57.28;
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Class: BAC ends.
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Best Local Similarity 57.2
Matches 147; Conservative
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                                                                                                                                                                         Anopheles.
           вн391959
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                                                                                                                                                                                                                                                                                                             Fax: 81-3-5449-5410
Email: jwatanab@manage.ims.u-tokyo.ac.jp
Suzuki/Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
Suzuki/Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDWA library Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
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AG-ND-180F9.TF ND-TAM Anopheles gambiae genomic clone AG-ND-180F9,
DNA sequence.
                                                                                                                        CDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 ATAGTAACAACAATAATAATAATAATAATAATAATAATAATAGTAACAATAATAATA 356
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malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                               Institute of Medical Science
The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan
191: 81-3-5449-5378
                                                                                         Watanabe, J., Sasaki, M., Suzuki, Y. and Sugano, S. Gruft-malaria: a database for a full-length enriched from human malaria parasite, plasmodium falciparum Nucleic Acids Res. 29 (1), 70-71 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dD_xrel___conc...
/clone=1xPfn2783.
/clone=1xb="Sugano Malaria cDNA library"
/dev_stage="erythrocytic stage" 3 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Plasmodium falciparum"
/strain="3D7"
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Pred. No. 0.00012;
0; Mismatches 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:5833"
                                                                                                                                                                                                          Contact: Junichi Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.7%;
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GSS 23-JUN-1999
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Sheared DNA-27K23.TR Sheared DNA Trypanosoma brucei genomic clone
Sheared DNA-27K23, DNA sequence.
1363 taatggtcaaattggcgtagatggaaaaattattagtgctaacagtaatacaaccagtgg 1422
                                                                                1423 ctcgacaaatcaagaatcatctgctactaacaatactgaaaatgctgttgttaatgaaag 1482
                                                                                                                                                                                                                                                     1543 tgaaaatgctgttgttaatgaaaacaaaaatactaacaacaacagaaaacgataatagtca 1602
                                                                                                                                                                       DEFINITION
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Gaps ö

Length 773;

Neoteleostei;

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Direct Submission
Submitted (12.APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                   CNSO4KUS 541 bp DNA linear GSS 21-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 117023 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotta, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Acanthopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; 1 (bases 1 to 541)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 541)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
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/db_xref="taxon:99883"
/clone="117023"
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48.7%; Pred. No. 0.00023;
ive 26; Mismatches 117;
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El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adms, M.
Determination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA, library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pUC18; Site_1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU92/74 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun
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4 c 79 g 134 t
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Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
MANA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: Mi3-Reverse
Class::shotgun.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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Pred. No. 0.00016;
0; Mismatches 123;
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/strain="TREU9274 GUTat 10.1"
/db_xref="taxon:569!"
/clone="Sheared DNA-27K23"
/clone_lib="Sheared DNA-27K23"
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Other_GSSs: Sheared DNA-27K23.TF
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/organism="Trypanosoma bruce;"
/strain="Trypanosoma bruce;"
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/db_xref="taxon:5691"
/clone="Sheared DNA-27123"
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/clone="Sheared DNA-17123"
/clone="She
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Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared

DNA library constructed at TiGR. Clones will be available for

distribution through ATCC. Sheared DNA end sequences search page:

http://www.tigr.org/tdb/mdb/tbdb/.
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Trypanosoma.
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58.1%; Pred. No. 0.00022;
tive 0; Mismatches 101; Indels 0.
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AUTHORS
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I (bases 1 to 560)

El-Sayed. N., Zabao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.

Praser, C. and Adams, M.

Determination of Clone end sequences from Trypanosoma brucei GuTat

10.1 sheared DNA library

Unpublished (1999)

Other_CSSS: Sheared DNA-3M5.TF

Contact: Najib M. El-Sayed

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Email: nelsayed@tigr.org

Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared

DNA library constructed at TIGR. Clones will be available for distribution through ATC. Sheared DNA end sequences search page:

Seq primer: M13-Reverse

Class: Shotgun.

Shotgun.

Tonation.
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/organism="Trypanosoma bruce;"
/strain="Trypanosoma bruce;"
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/note="Vector: pUG18; Site_1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MN.
Genomic DNA isolated from a cloned population of Trypanosoma bruce! (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and venter, J.C. (Makking small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University
Sheared DNA-3M5.TR Sheared DNA Trypanosoma brucei genomic clone Ab658275.
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Similarity 58.5%; Pred. No. 0.00024;
8; Conservative 0; Mismatches 98; Indels 0;
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Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                        Sequence:
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Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli		Length 3305;
28 50.2 1.1 5116 2 US-08-469-880-1 29 50.2 1.1 5116 2 US-08-728-470-1 31 50.2 1.1 5116 2 US-08-728-470-1 32 50.2 1.1 5116 2 US-08-728-470-1 33 50.2 1.1 9171 1 US-08-318-681-5 34 50.2 1.1 9171 1 US-08-31-83-5 35 50.2 1.1 9171 2 US-08-617-697-5 36 50.2 1.1 9171 2 US-08-616-860-5 37 50.2 1.1 9171 2 US-08-616-697-5 38 50.2 1.1 9171 2 US-08-617-697-5 39 49.4 1.1 1956 4 US-08-719-641-5 40 48.2 1.0 665 2 US-08-758-896B-1 41 48.2 1.0 665 2 US-08-119-1258-2 42 47.8 1.0 5852 1 US-08-119-1258-2 43 47 1.0 6124 4 US-08-119-1258-2 44 66.6 1.0 1431 4 US-08-618-11	RESULT 1  US-09-068-043-1  Sequence 1, Application US/09068043  Patent No. 6048694  Patent No. 6048694  Patent No. 6048694  Patent NO. 6048694  Patent NO. 6048694  TITLE OF INVENTION: POSITIVE SELECTION  TITLE OF INVENTION: POSITIVE SELECTION  TITLE OF INVENTION: POSITIVE SELECTION  TITLE OF INVENTION: POSITIVE SELECTION  TITLE OF INVENTION: POSITIVE SELECTION  TITLE OF INVENTION: POSITIVE SELECTION  TITLE OF INVENTION: POSITIVE SELECTION  TITLE OF INVENTION: POSITIVE SELECTION  STREET: 1007 MARKET STREET  COMPRESSEE: COMPANY  STREET: 1007 MARKET STREET  COMPANY  STREET: 1007 MARKET STREET  COMPUTER: DELAMARE  COMPUTER: DELAMARE  COMPUTER: LIST DELAMARE  COMPUTER: LIST DELAMARE  COMPUTER: LIST DELAMARE  COMPUTER: JEM PC COMPATIBLE  COMPUTER: JEM PC COMPATIBLE  COMPUTER: JEM PC COMPATIBLE  COMPUTER: JEM PC COMPATIBLE  COMPUTER: JEM PC COMPATIBLE  COMPUTER: JEM PC COMPATIBLE  COMPUTER: JEM PC COMPATIBLE  COMPUTER: JEM PC COMPATIBLE  COMPUTER: JEM PC COMPATIBLE  COMPUTER: JEM PC COMPATIBLE  COMPUTER: JEM PC COMPATIBLE  COMPUTER: JEM PC COMPATIBLE  COMPUTER: JEM PC COMPATIBLE  COMPUTER: JEM PC COMPATIBLE  COMPUTER: JEM PC COMPATIBLE  COMPUTER: JEM PC COMPATIBLE  COMPUTER: JEM PC COMPATIBLE  COMPUTER: JEM PC COMPATION:  FILING DATE: NOVEMBER: GP-0066, 201  FILING DATE: NOVEMBER: GP-0066, 201  FELEPHONE: 302-773-0164  SEQUENCE CHARACTERISTICS:  LENGTH: 3305 base pairs  TREE. TOPOLOGY: Jinear  MOLECULE TYPE: NON OF SECULE OF SECULE OF SECULE AND SECULE SECULE AND SECULE SECULE SECULE SECULE SECULE SECULE SECULE  HYPOTHETICAL: NO  SECULE TYPE: NON OF SECULE S	Query Match 1.6%; Score 75; DB 3; Le Best Local Similarity 50.7%; Pred. No. 9.8e-09;

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NAME/KEY: single stranded DNA replication origin LOCATION: 1423..1894 LDENTHICATION METHOD: By homology to U46017 OTHER INFORMATION: mutation T -> C 1658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: IncC
LOCATION: 3070..3320
IDENTIFICATION METHOD: By homology to U51113
OTHER INFORMATION: insertion 33 bases 3038..3071
                                                                                                                                                                                                                          Homology with X06404 compl (411..1668)
                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Tn1000'sright end
LOCATION: complement 1332..1371
IDENTIFICATION METHOD: blastn against X60200)
                                                                                                                                                                                                                                             LOCATION: 9..1266
IDENTIFICATION METHOD: blastn against X06404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1423..1894
IDENTIFICATION METHOD: blastn against U46017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAME/KEY: Homology with U51113 (2382..6997)
LOCATION: 1896..6544
IDENTIFICATION METHOD: blastn against U51113
                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION METHOD: By homology to X06404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      By homology to U51113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        By homology to U51113
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OTHER INFORMATION: Described in seqID 17
                                                                                                                                                                                                                                                                                                         Kanamycin resistance gene CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homology with U46017 (1-472) 1423..1894
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                                                                                                                            Cloning vector pGenDEL
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LOCATION: 2897.2918
OTHER INFORMATION: Described in
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OTHER INFORMATION: Described in
FATURE:
                                                              TOPOLOGY: CIRCULAR
MOLECULE TYPE: synthetic DNA
ORIGINAL SOURCE:
ORGANISM: Cloning vector po
        : 10317 base pairs
NUCLEIC ACID
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LOCATION: 1972..2188
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
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LOCATION: 3655..4821
IDENTIFICATION METHOD:
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                                               DOUBLE
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3043..3059
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2903..3034
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1..10317
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                                               STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2687 CAGAAGCTTCAGCAGAGCGCTAAAAAACGCGA---TGCTGAGTTAGCGAACGGCGCCCTC 2743
                                     2132 acaaatgtgttccaagaatggtcaggttcagctattgtaaatgatgatggtacaattcaa 2191
                                                                                                                  2192 ctattttcacctcaaatgatacgtctgattacaagttgaatgatcaacgccttgctacc 2251
                                                                                                                                                     2333 TTATICTACAC-----TGACTATICCGGTAAACATTACGGCAAACAAAGCCTGACAACA 2386
                                                                                                                                                                                               2312 caagititgiitgaaggigatgattgattcactaccaaactiaigaacaaitcgcaaacggc 2371
                                                                                                                                                                                                                                                                                                                                                         2372 aaagatogtgaaaatgatgattactgottacgtgacocacacgttgttcaattagaaaat 2431
                                                                                                                                                                                                                                                                                                                                                                                              2507 GGCAATTATACATCCGCCGACAACCATACGCTGAGAGACCCTCACTACGTTGAAGACAAA 2566
      12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2489 gaccaaatttataattgggctaactatggtggcgatgatgccttcaatattaagagttcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09058746
Patent No. 6022716
GENERAL INFORMATION:
APPLICANT: Ilya Chumakov
APPLICANT: HIVOAKI Tanaka
TITLE OF INVENTION: High Throughput DNA sequencing vector
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
    Mismatches 245; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,746
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NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/CDCKET NUMBER: GENS!
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
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COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy Disk
COMPUTER: IBM PC: compatible
OPERATING SYSTEM: Win95
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
Matches 264; Conservative
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CITY: San Diego
STATE: California
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US-09-058-746-1/c
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IDENTIFICATION METHOD: By homology to M77789
OTHER INFORMATION: site Scal 10029 - 10034
OTHER INFORMATION: site Scal 10029 - 10034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME, KEY: Homology with J01636 (complement 1158..1465) LOCATION: 9298..9623 IDENTIFICATION METHOD: blastn against J01636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MANGATION: CDS levansucrase gene
LOCATION: complement 7379..8800
IDENTIFICATION METHOD: By homology to X02730
OTHER INFORMATION: mutation T -> C 7466
OTHER INFORMATION: mutation T -> C (Asn -> Asp) 8347
OTHER INFORMATION: mutation T -> C (Asn -> Asp) 8347
OTHER INFORMATION: mutation T -> C 8600
OTHER INFORMATION: mutation G -> A (Ala -> Val) 8772
NAME/KEY: Homology with J01688 (complement 175..819)
LOCATION: 6574..7218
LIDENTIFICATION METHOD: blastn against J01688
OTHER INFORMATION: mutation A -> G 7096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Homology with X02730 (complement 37..1959)
LOCATION: 7305..9227
IDENTIFICATION METHOD: blastn against X02730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS alpha peptide beta-galactosidase LOCATION: complement 9276..9497
IDENTIFICATION METHOD: By homology to J01636
                                                                                                        NAME/KEY: CDS streptomycin sensitivity gene LOCATION: complement 6716.7090
IDENTIFICATION METHOD: By homology to J01688
OTHER INFORMATION: mutation A -> 6 6728
OTHER INFORMATION: mutation G -> C 6821
OTHER INFORMATION: mutation T -> C 7013
OTHER INFORMATION: mutation T -> A 7058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION METHOD: blastn against M77789
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                                                                                                                                                                                                                   OTHER INFORMATION: mutation C -> T 6866
OTHER INFORMATION: mutation T -> C 7013
OTHER INFORMATION: mutation T -> A 7058
FEATURE:
LOCATION: 7155..7174
OTHER INFORMATION: Described in seqID 12
                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SP6
LOCATION: 7230..7248
OTHER INFORMATION: Described in seqID 13
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LOCATION: 8711..8731
OTHER INFORMATION: Described in seqID 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Tn1000's left end
LOCATION: 7252..7291
IDENTIFICATION METHOD: blast (x60200)
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complement 9603..9630
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9289..9314
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9461..9475
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NAME/KEY:
LOCATION:
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LOCATION:
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7849 CTAAACGATGATTACA-----CACTGAAAAAGTGATGAAACCGCTGATTGCATCTAAC 7796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8261 ----TGATTTCTCCGGTAAACATTACGGCAAACACACTGACAACTGCACAACGTTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8086 TCAGGCGACAACCATACGCTGAGAGATCCTCACTACGTAGAAGATAAAGGCCACAAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2501 aattgggctaactatggtggcgatgatgccttcaatattaagagttccttcaagcttttg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7795 ACAGTAACAGATGAAGTGGCGCGAACGTCTTTAAAATGAACGCCAAATGGTATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2444 cttgtattcgaagctaatactgggacagaagat...taccaaagtgacgaccaaatttat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2681 ttgatggcttgcgatgaggtannnnnnaagcttggtgataagtattatctctccgta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCACTGA-------CTCCCGCGATCAAAATGACGATTGACGCATTACGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2741 actcgtgtaagtcgtggttccgatcgtgaattaaccgctaaggataacacaatcgttggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 10317;
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OTHER INFORMATION: Site PmlI 10038 - 10043
OTHER INFORMATION: CLONING SITES 10031 - 10041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.5%; Score 69.4; DB 3;
Best Local Similarity 47.4%; Pred. No. 3.4e-07;
Matches 381; Conservative 0; Mismatches 392;
                                                                                                                                                           NAME/KEY: OS1
LOCATION: 10009..10026
FORTHER INFORMATION: Described in seqID 10
NAME/KEY: OR1
                                                                                                                                                                                                                                                                               LOCATION: complement 10046..10062
OTHER INFORMATION: Described in seqID
                                                                                                                                                                                                                                                                                                                                                     : NAME/KEY: orilrr

: LOCATION: complement 10182..10202

: OTHER INFORMATION: Described in seqID

US-09-058-746-1
                                                                NAME/KEY: OTILRd
LOCATION: 9856..9881
OTHER INFORMATION: Described in seqID
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NAME/KEY: OriS
LOCATION: 1972..2188
IDENTIFICATION METHOD:
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LOCATION: 2903..3034
IDENTIFICATION METHOD:
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LOCATION: 4821..5792
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
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LOCATION:
Sequence 1. Application US/09438142

Patent No. 6258571

GENERAL INFORMATION:
APPLICANT: Hivoaki Tanaka
TITLE OF INVENTION: High Throughput DNA equencing vector
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Homology with X06404 compl (411..1668)
LOCATION: 9..1266
IDENTIFICATION METHOD: blastn against X06404
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: single stranded DNA replication origin
LOCATION: 1423..1894
IDENTIFICATION METHOD: By homology to U46017
OTHER INFORMATION: mutation T -> C 1658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAME/KEY: Th1000'sright end
LOCATION: complement 1332..1371
IDENTIFICATION METHOD: blastn against X60200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Homology with U46017 (1-472)
LOCATION: 1423..1894
IDENTIFICATION METHOD: blastn against U46017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Kanamycin resistance gene CDS
LOCATION: 142..957
IDENTIFICATION METHOD: By homology to X06404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: GENSET.015C1
TELECOMMUNICATION INFORMATION:
TELEFRONE: (619) 235-6156
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPPOLOGY: circular
MOLECULE TYPE: SYNTHATIC DNA
ONLINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,142
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Cloning vector pGenDEL
                                                                                  COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: pGendel
LOCATION: 1.10317
                                                                                                                                                                                       RESULT 3
US-09-438-142-1/c
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NAME/KEY: Homology with J01688 (complement 175..819)
LOCATION: 674..7218
LIDENITEMENT 6574..7218
LIDENITEMENT METHOD: blastn against J01688
OTHER INFORMATION: mutation A -> G 7096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Homology with X02730 (complement 37..1959)
LOCATION: 7305.:9227
IDENTIFICATION METHOD: blastn against X02730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: IncC
LOCATION: 3070..3320
IDENTIFICATION METHOD: By homology to U51113
OTHER INFORMATION: insertion 33 bases 3038..3071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS streptomycin sensitivity gene LOCATION: complement 6716.7090
LOCATION: complement 6716.7090
LOCATION: complement 6716.7090
OTHER INFORMATION: mutation A -> 6 6728
OTHER INFORMATION: mutation G -> C 6821
OTHER INFORMATION: mutation C -> 7 6866
OTHER INFORMATION: mutation T -> C 7013
OTHER INFORMATION: mutation T -> C 7013
FEATURE:
LOCATION: 7155.7174
COCATION: 7155.7174
COCATION: 7155.7174
NAME/KEY: Homology with U51113 (2382..6997)
LOCATION: 1896..6544
IDENTIFICATION METHOD: blastn against U51113
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 3655.4821
IDENTIFICATION METHOD: By homology to U51113
OTHER INFORMATION: mutation G -> A 3878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: ParC
LOCATION: 5865..6382
IDENTIFICATION METHOD: By homology to U51113
                                                                                                                                                                                                                                                                                                                                                                                                By homology to U51113
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                                                                                                                                                                                                                       NAME/KEY: repELR
LOCATION: 2897..2918
OTHER INFORMATION: Described in seqID 16
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LOCATION: 3043..3059
OTHER INFORMATION: Described in seqID 17
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OTHER INFORMATION: Described in seqID 15
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LOCATION: 7230..7248
OTHER INFORMATION: Described in seqID 13
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LOCATION: 7252..7291
IDENTIFICATION METHOD: blast (X60200)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2144 caagaatggtcaggttcagctattgtaaatgatgatggtacaattcaactatttttcacc 2203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                replication origin
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47.4%; Pred. No. 3.4e-07;
tive 0; Mismatches 392; Indels
                                                                                                                                                                                                                                                                   NAME/KEY: Homology with J01636 (complement 1158..1465) LOCATION: 9298..9623 IDENTIFICATION METHOD: blastn against J01636
                                                                                                                                                8772
NAME/KEY: CDS levansucrase gene
LOCATION: complement 7379.8800
IDENTIFICATION METHOD: By homology to X02730
OTHER INFORMATION: mutation T -> C 7466
OTHER INFORMATION: mutation A -> G 7739
OTHER INFORMATION: mutation T -> C (Asn -> Asp) 8
OTHER INFORMATION: mutation T -> C 6600
OTHER INFORMATION: mutation G -> A (Ala -> Val) 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: high copy-number double-stranded DNA 1
LOCATION: complement 9629..10315
IDENTIFICATION METHOD: By homology to M7789
OTHER INFORMATION: mutation C -> T 9803
OTHER INFORMATION: site Scal 10029 - 10034
OTHER INFORMATION: site Pml1 10038 - 10043
OTHER INFORMATION: CLONING SITES 10031 - 10043
                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS alpha peptide beta-galactosidase LOCATION: complement 9276..9497
IDENTIFICATION METHOD: By homology to J01636
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 9629.10315
IDENTIFICATION METHOD: blastn against M77789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homology with M77789 (1889..2576)
9629..10315
                                                                                                                                                                                                   LOCATION: 8711..8731
OTHER INFORMATION: Described in seqID 14
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OTHER INFORMATION: Described in seqID 10
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LOCATION: complement 10046..10062
OTHER INFORMATION: Described in seqID 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: complement 10182..10202
COTHER INFORMATION: Described in seqID
US-09-438-142-1
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OTHER INFORMATION: Described in seqID
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complement 9603..9630
                                                                                                                                                                                                                                                                                                                                                                                                                               primer HE1
complement 9465..9479
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9289..9314
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Matches 381; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer HE2
9461..9475
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                                                                                                                                                                                    NAME/KEY: SLR3
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LOCATION:
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LOCATION:
FEATURE:
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LOCATION:
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LOCATION:
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GENERAL INFORMATION:
APPLICANT: Jenkins, Mark C.
APPLICANT: Fever, Ronald
APPLICANT: Trout, James
TITLE OF INVENITION: Cloning and Expression of a DNA Sequence Encoding A 41
Patent No. 6277973
TITLE OF INVENITON: kDa Cryptosporidium parvum Oocyst Wall Protein
FILE REFERENCE: 0046.99
                                                                                                                                                                                                                                                                                                                                                                                                         2561 aataataagaaggatcgtgaattggctggtttagctaatggtgcacttggtatcttaaag 2620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2621 ctcactaacaatcaaagtaagccaaaggttgaagaagtatactcaccattggtatctact 2680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7849 CTAAACGATGATTACA-----CACTGAAAAAGTGATGAAACCGCTGATTGCATCTAAC 7796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2681 ttgatggcttgcgatgaggtannnnnnaagcttggtgataagtattatctcttctccgta 2740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2861 aataactcaggtgtcgtattaactgcatcagtacctgcaaactggcgtactgctacttat 2920
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                                                                                                                                                                                                                                                                                                                                               8086 TCAGGCGACAACCATACGCTGAGATCCTCACTACGTAGAGATAAAGGCCACAAATAC 8027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7966 AACAAAGCATACTATGGCAAAAGCACATCATTCTTCCGTCAAGAAAGTCAAAAACTTCTG 7907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7735 TTCACTGA------CTCCCGCGGATCAAAATGACGATTGACGCATTACGTCT 7688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7687 AACGATATITACATGCTTGGTTATGTTTCTAATTCTTTAACTGGCCCATACAAGCCGCTG 7628
----TGATTTCTCCGGTAAACATTACGGCAAACAAACACTGACAACTGCACAGTTAAC 8207
                                                    2264 cttaatgttgatgataacggtgtttcaatcaagagtgttgataattatcaagttttgttt
                                                                                                                                                                                                              2384 aatgatgattactgcttacgtgacccacacgttgttcaattagaaaatggtgatcgttat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2501 aattgggctaactatggtggcgatgatgccttcaatattaagagttccttcaagcttttg
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CURRENT FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 4
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2921 tectactatgeagtacetgtage 2943
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Patent No. 6277973
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; ORGANISM: Cryptosporidium parvum
US-09-451-117-1
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                                                                                                      1287 ttgtaaccgctcatgctgatcaagtagaaagtaacaattacaacggtgttgctgaagtta 1346
                                                                                                                                                                                                                      1347 atactgaacgtcaagctaatggtcaaattggcgtagatggaaaaattattagtgctaaca 1406
                                                                                                                                                                                                                                                                                                                                  1407 gtaatacaaccagtggctcgacaaatcaagaatcatctgctactaacaatactgaaaatg 1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1467 ctgttgttaatgaaagcaaaaatactaacaatactgaaaatgctgttgttaatgaaaaca 1526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aaaatactaacaatactgaaaatgctgttgttaatgaaaacaaaaatactaacaacacag 1586
                                                                                                                                          Gaps
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   Length 740;
                                                      0; Mismatches 156; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATION:
COMPUTER: IBM PC COMPATION:
COMPUTER: IBM PC COMPATION:
COMPUTER: IBM PC COMPATION:
COMPUTER: COMPATION:
COMPUTER: COMPATION:
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Score 64.4; DB 4;
Pred. No. 1.9e-06;
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Fatent No. 5962297
GENERAL INCOMPATION:
APPLICANT: TSUSAKI et al.
TITLE OF INVENTION: POLYPEPTIDE HAVING -F
TITLE OF INVENTION: ACTIVITY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.4%;
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                     Best Local Similarity 50.3
Matches 158; Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-08-870-827-4
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Query Match
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2299 tgitgataattatcaagtittgittgaaggtgatggatttcactaccaaacttatgaaca 2358
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                       Length 1365;
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                                                                                                       Indels
    Score 61.2; DB 2;
Pred. No. 1.5e-05;
0; Mismatches 178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: TSUSAKI et al.
TILLE OF INVENTION: POLYPEPTIDE HAVING -FRUCT
TITLE OF INVENTION: ACTIVITY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
ADBRESSE: ADDRESSE:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 170,630/1996
FILING DATE: 10-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08870827
Patent No. 5962297
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
1.3%;
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TELEPHONE: 202-628-5197
                                               Best Local Similarity 50.0 Matches 181; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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         Query Match
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Patent No. 5849306
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Miler, Louis H.
APPLICANT: Miler, Louis H.
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ENTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCES: 37
CORRESPONDENCE ADDRESS:
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Best Local Similarity 50.0%; 'Pred. No. 1.8e-05; Matches 181; Conservative 0; Mismatches 178;
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620 Newport Center Drive 16th Floor
                                                               ORGANISM: Bacillus sp.
INDIVIDUAL ISOLATE: V230 (FERM BP-5054)
                                                                                                                                LOCATION: 1.360
IDENTIFICATION METHOD: E
NAME/KET: signal peptide
LOCATION: 361.456
IDENTIFICATION METHOD: S
NAME/KET: mat peptide
LOCATION: 457..1821
              TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                    IDENTIFICATION METHOD:
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US-08-870-827-5
STRANDEDNESS: double
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LOCATION: 1822..2408
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| AT 1405
                                                                                                                    NAME/KEY:
                                                                  ORGANISM:
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US-08-568-459A-3
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2670 AAGATCAAAATAGTGATGAATCGGAAGAAACTGTAGTAAATCATATATCAAAAGTCCAT 2729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.3%; Score 59.8; DB 2;
Best Local Similarity 46.0%; Pred. No. 5e-05;
Matches 202; Conservative 0; Mismatches 237;
                                                                                                                                                      APPLICATION NUMBER: US/08/568,459A FILING DATE: 07-DEC-1995 CLASSIFICATION: 435
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
US-08-568-459A-3
                                                                                                                                                                                                        CLASSIFICATION: 43.2
ATTORNEY FACENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REPERBENCE/DOCKET NUMBER: NH12
TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 235-856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4507 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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STRANDEDNESS: single
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3030 GTAATTCTGATAATGTTCAACAGTCTGGAGGAATTGTTAATATGAATGTTGAGAAACA3089
              1668 ctcaagctgctaaggctgttcaaaatgccaagattgatgccggtagtttaacagatgatc 1727
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                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Do Wilde, Michel
APPLICANT: TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmodium and HBSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
STREET: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/760,797A FILING DATE: 04-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/442,612
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         Sequence 2, Application US/08760797A
Patent No. 5928902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33,833
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                    1728 aaattaatgaattaaataa 1746
                                                                                                                              3090 TAAAAGATACTTTAGAAAA 3108
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REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Best Local Similarity
Matches 207; Conserva
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US-08-760-797A-2
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                                          APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.3%; Score 59.8; DB 2;
46.0%; Pred. No. 5e-05;
tive 0; Mismatches 237;
                                                                                                                                                                                                 ADDRESSEE: Knobbe Martens Olson & Bear STREET: 620 Newport Center Drive 16th Floor STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH121.001CP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/487,826B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: ISTRAETON UNDBER: 29,655
REGERATION UNDBER: 01,655
REFERENCE/DOCKET NUMBER: NIH1;
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 235-0176
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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N: 435
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 202; Conservative
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1280 AAATGCAAACCCCAATGCAAATCCTAATAAAAACAATCAAGGTAATGGACAAGGTCACAA 1339
                                                           1693 tgccaagattgatgccggtagtttaacagatgatcaaattaatgaattaaataagattaa 1752
                                                                                                 1340 TATGCCAAATGACCCAAACCGAAATGTAGATGAAATGCTAATGCCAACAATGCTGTAAA 1399
                                                                                                                                       1753 cttctctaagtctgctgaaaagggtgcaaaattgacctttaaggacttagagggattgg 1812
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Pred. No. 0.00019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmodium and HBsAG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SMITHKINE Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,929B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.2%; Score 57.2; Di
nilarity 47.7%; Pred. No. 0.000
Conservative 0; Mismatches
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REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: B45015-1FWC2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,797
FILING DATE: 04-DEC-1996
APPLICATION NUMBER: 08/42,612
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08932929B Patent No. 6169171 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                   1873 caagaatatgcctg 1886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                           1520 TAGAATAAAGCCTG 1533
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STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity
Matches 207; Conserva
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cacagaaaacgataatagtcaattaagttaactaataatgaacaaccatcagccgctac 1641
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                                                       1522 aaacaaaaatactaacaatactgaaaatgctgttgttaatgaaaacaaaatactaacaa 1581
                                                                                                                                                                                                                                                      1280 AATIGCAAACCCCAATIGCAAATCCTAATAAAACAATCAAGGTAATGGACAAGGTCACAA 1339
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Patent No. 5849573
RENERAL INFORMATION:
APPLICANT: Stewart, Thomas S
APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Nixon & Vanderhye PC
STREET: 1100 No. 5849573th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
CUNTRY: USA
IP: 22201-4714
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-Jul-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.09
REFRENCE/DOCKET NUMBER: 47-81
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: single
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CLASSIFICATION:
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SEQ ID NO 1
LENGTH: 1631
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US-09-118-319-1
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                                                                                     1609
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Sequence 1, Application US/09150741

Sequence 1, Application US/09150741

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate

PATILE OF INVENTION: Synthetase II

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/150,741

CURRENT APPLICATION NUMBER: PL6380

EARLIER APPLICATION NUMBER: PL6380

EARLIER APPLICATION NUMBER: PL6380

EARLIER FILING DATE: 1993-12-02

EARLIER FILING DATE: 1993-12-02

EARLIER FILING DATE: 1993-12-02

EARLIER FILING DATE: 1995-07-06

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PATENTIN Ver. 2.0
                                                                                        1429 aaatcaagaatcatctgctactaacaatactgaaaatgctgttgttaatgaaagcaaaaa 1488
                                                                                                                 1489 tactaacaatactgaaaatgctgttgttaatgaaaacaaaaatactaacaatactgaaaa 1548
                                                                                                                                                                gttaactaataatgaacaaccatcagccgctactcaagcaaacttgaagaagctaaatcc 1668
                                                                                                                                                                                                                                                                         tcaagctgctaaggctgttcaaaatgccaagattgatgccggtagtttaacagatgatca 1728
                                                                                                                                                                                                                                                                                                                                 TITAAGTAGTGAAGAATIGAATACTGATGAGTATGATGATGATGATATTATTATGATGAAGA 6546
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                                          Length 8920;
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                                       Score 56.6; DB 2; Length 8
Pred. No. 0.00039;
0; Mismatches 214; Indels
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Pred. No. 0.00039;
0; Mismatches 214;
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                                                     46.48;
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1.2%;
Best Local Similarity 46.4%;
Matches 185; Conservative
                                    Query Match 1.2%
Best Local Similarity 46.4%
Matches 185; Conservative
US-08-446-855A-1
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APPLICANT: Li, Xin-Liang
APPLICANT: Chen, Huizhong
APPLICANT: Chen, Huizhong
APPLICANT: Liungdahl, Lars G.
TITLE OF INVENTION: Orpinomyces Cellulase CelF Protein and Coding Sequences
FILE REFERENCE: 33-98sequence listing
CURRENT APPLICATION NUMBER: US/09/118,319
CURRENT FILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                               1729 aattaatgaattaaataagattaacttctctaagtctgctgaaaagggtgcaaaattgac 1788
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; Patent No. 6114158
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 48.0
Matches 160; Conservative
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LOCATION: (187)..(297)
US-09-118-319-1
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1129 CAAACCCCAATGCAAATCCTAATGCAAATCCTAATGCCAATCCAAATGCAAATCCAAATG 1188
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                                                                                                               1429 AATATTTAAACAAAATACAAAAATTCTCTTTCAACTGAATGGTCCCCATGTAGTGTAACTT 1488
1734 atgaattaaattaagattaacttctctaagtctgctgaaaagggtgcaaaattgaccttta 1793
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                                         1369 ATGCCAACAGTGCTGTAAAAATAATAATAACGAAGAACCAAGTGATAAGCACATAAAAG
                                                                                      aggacttagaggggattggtaatgctattgttaagcaagatccacaatatgctattcctt
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Pred. No. 0.00052;
0; Mismatches 231;
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmodium and HBSAG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,929B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: SmithKline Beecham Corporation 709 Swedeland Road
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,797
FILING DATE: 04-DEC-1996
APPLICATION NUMBER: 08/42,612
FILING DATE: 17-MAY-1995
ATTORNEY/AGBNI INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REGISTRATION NUMBER: 33,833
                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08932929B Patent No. 6169171
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LENGTH: 3504 base pairs
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diskette
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COMPUTER READABLE FORM:
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Matches 213; Conserva
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US-08-932-929B-4
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US-08-932-929B-4
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STATE: P.
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                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,797A ·
FILING DATE: 04-DEC-1996
CLASSIFICATION: 435
                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Chen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmodium and HBSAG
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkiine Beecham Corporation
                                                                                                                                                                                                                                               STATE: PA
COUNTRY: USA
ZITE: TO
      686 catcttaaggctgctggttctaaaactgttgta 718
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/442,612
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
                                                                                                        Sequence 4, Application US/08760797A
Patent No. 5928902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.2%;
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.2
Best Local Similarity 47.0
Matches 213; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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US-08-760-797A-4
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US-08-760-797A-4
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #21590.
                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
         AAS92589
AAS85839
AAS86014
                                      AAS87349
AAS86020
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AAS86037
AAS65782
AAS6429
AAS6820
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AAS84054
AAS68494
AAS85800
AAS86022
AAS87359
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AAS85792
AAS86019
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AAS84506
AAS85069
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2000US-0649167
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Drmanac RT, Liu C,
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P-PSDB; ABG21599.
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  WO200175067-A2.
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23-AUG-2000;
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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
| SIDSI/gcgdata/geneseq-geneseqn-embl/NA1986.DAT:*
| SIDSI/gcgdata/geneseq-geneseqn-embl/NA1980.DAT:*
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                    ; Search
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first 45 summaries
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787 tacggcggcggcacgaacttcttccgtaaagaaagccagaagcttcagcagagcgctaaa

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in casponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and annowed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostic coding sequences of the invention.
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                                                                                                   Claim 1; SEQ ID No 21590; 103pp; English.
                                                        biodiversity
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3; 2155 2215 2275 2395 1976 gtatctaattacatgggttatcaactagttattgctatgatgggtattccaaattcgcca 2035 313 atgacacatcaatctacatgttttatcaaaagctggaaaaacgcgggccgtgtctttaaa 372 909 Gaps 2036 actggagataatcatatctatctttacaacaagtatggtgataatgacttttctcat 2096 tggcgcaatgcaggttcaatctttggaactaaagaaacaaatgtgttccaagaatggtca gacagcgataagttcgacgccaacgatccgatcctgaaagatcagacgcaagaatggtcc ggttcagctattgtaaatgatgatggtacaattcaactatttttcacctcaaatgatacg tctgattacaagttgaatgatcaacgccttgctaccgcaacattaaaccttaatgttgat 547 gatgacacactcaaaatcaacggagtggaagatcacaaaacgatttttgacggagacgga tttcactaccaaacttatgaacaattcgcaaacggcaaagatcgtgaaaatgatgattac 2396 tgcttacgtgacccacacgttgttcaattagaaaatggtgatcgttatcttgtattcgaa catacgctgagagaccctcactacgttgaagacaaaggccataaataccttgtattcgaa 607 aaaacatatcagaacgttcagcagtttatcgatgaaggcaattatacatccggcgacaac gctaatactgggacagaa---gattaccaaagtgacgaccaaatttataattgggctaac tccggtaaacattacggcaaacaaagcctgacaacagcgcaggtaaatgtgtcaaaatct 12; DB 23; Length 2079; Query Match
1.9%; Score 88.6; DB 23; Length:
Best Local Similarity 48.9%; Pred. No. 5.9e-09;
Matches 331; Conservative 0; Mismatches 334; Indels 373 2156 2216 487 2276 2336 667 g ð 셤 ò 셤 ò q ò 셤 à g ò a à g à g

Sequence 2079 BP; 461 A; 475 C; 433 G; 710 T; 0 other;

tatggtggcgatgatgccttcaatattaagagttccttcaagcttttgaataataagaag 2572

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polypeptide (II) sequences. (II) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in disorders, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at Itp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human
                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                           novel human diagnostic protein #21802.
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2000US-0649167
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                             Indels 12;
        Length 2079;
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      Score 88.6; DB 23;
Pred. No. 5.9e-09;
0; Mismatches 334;
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                Best Local Similarity 48.9
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48.9%; Pred. No. 5.9e-09;
iive 0; Mismatches 334;
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                                                                                                                                                                                                                                                         Claim 1; SEQ IQ No 23146; 103pp; English.
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Best Local Similarity
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                                                                                    Liu C,
                                                  (HYSE-) HYSEQ INC
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31-MAR-2000;
23-AUG-2000;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical smaging of sites expressing (II). (I) and (II) are useful for treating
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
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disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.WIPO.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                .1976 gtatctaattacatgggttatcaactagttattgctatgatgggtattccaaattcgcca 2035
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0; Mismatches 334;
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                                                                                             Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:238
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                                                                                                                                                                                  Plasmodium falciparum; chromosome 2; human malaria parasite; antimalarial; malaria; protozoacide; infection; insecticide;
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07-NOV-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (VENT/) VENTER J C.
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                                                                                                                                                                                                                                                                                                                                                                                                              40200025728-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35-NOV-1998;
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaping of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations
                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #21854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 21854; 103pp; English.
                                                                                                      AAS86050 standard; cDNA; 3947 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0540217
2000US-0649167
                                                                                                                                                                               (first entry)
             560
WPI; 2001-639362/73.
P-PSDB; ABG21863.
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                                                                                                                                                                                                                                                                                                                                               WO200175067-A2.
                                                                                                                                                                                                                                                                                                              Homo sapiens.
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23-AUG-2000;
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responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human
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from WIPO
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food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                    458 ttattctacac----tgactattccggtaaacattacggcaaacaaagcctgacaaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                              diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                              Length 3947;
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                                                                                                                                                                                                           Indels
                                                                                                                         Sequence 3947 BP; 1081 A; 940 C; 894 G; 1031 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding novel human diagnostic protein #17231.
                                                                                                                                                                         Score 78.2; DB 23;
Pred: No. 1e-06;
0; Mismatches 248;
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                                                                                                                                                                           1.78;
50.98;
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                                                                                                                                                                        Query Match 1.7%
Best Local Similarity 50.9%
Matches 269; Conservative
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, colypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and call sequences. Ansofalpy-AAS94564 represent novel human call sequences of the invention.

Conterm the sequence data for this patent did not appear in the printed contermination of the printed contermination of the printed content is a content of the content of the printed content is patent did not appear in the printed content is patent did not appear in the printed content is patent did not appear in the printed content is patent and product of printed content in the printed content is patent and product of printed content in the printed content is patent and product of printed content in the printed content is patent and product of printed contents and product of printed contents of the printed contents and printed contents and printed contents and printed contents and printed contents and printed contents and printed contents and printed contents and printed contents and printed contents and printed contents and printed conte
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51.0%; Pred. No. 1.9e-06;
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                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 17231; 103pp; English.
                                                                                                                                    YT;
31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                  WPI; 2001-639362/73
                                                                                                                                  Drmanac RT, Liu C,
                                                                              (HYSE-) HYSEQ INC
                                                                                                                                                                                                              P-PSDB; ABG17240
                                                                                                                                                                                                                                                                                                                                          biodiversity
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
2549 ttcaagcttttgaataataagaaggatcgtgaattggctggtttagctaatggtgcactt 2608
               896 CAGAAGCTTCAGCAGAGCGCTAAAAAACGCGA---TGCTGAGTTAGCGAACGGCGCCCTC 840
                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                      2609 ggtatcttaaagctcactaacaatcaaagtaagccaaagg 2648
                                                                                                                                                                DNA encoding novel human diagnostic protein #21828.
                                                ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 21828; 103pp; English.
                                                                                                          BP.
                                                                                                AAS86024/c
ID AAS86024 standard; cDNA; 979
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                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167.
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                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                          Drmanac RT, Liu C,
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                                                                                                                                                                                   Human; chromosome
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Sequence 979 BP; 194 A; 251 C; 222 G; 312 T; 0 other;

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Antisense oligonucleotide for inhibiting human egg expression, comprises a sequence corresponding to a nucleotide sequence encoding a defined part of a human eg5 or its mutated form -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2549 ttcaagcttttgaataataagaaggatcgtgaattggctggtttagctaatggtgcactt 2608
                                                             2132 acaaatgtgttccaagaatggtcaggttcagctattgtaaatgatgatggtacaattcaa 2191
                                                                                                                                                                                                                     477 GCGCAGGTAAATGTGTCAAAATCTGATGACACTCAAAATCAACGGAGTGGAAGATCAC 418
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                                                                                                                                                                                                                                                                                                                                                  357 GGCAATTATACATCCGGCGACAACCATACGCTGAGAGACCCTCACTACGTTGAAGACAAA 298
                                                                                                                                                                                                                                                                                                                                                                                                               297 GGCCATAAATACCTTGTATTCGAAGCCAACAGGGAACAGAAAACGGATACCAAGGCGAA 238
                                                                                           591 AAAGATCAGACGCAAGAATGGTCCGGTTCTGCAACTTTTACATCTGACGGAAAATCCGT 532
                                                                                                                                                        531 TTATTCTACAC-----TGACTATTCCGGTAAACATTACGGCAAACAAAGAGCTGACAACA 478
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                                       Gaps
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                                                                                                                          2192 ctattttcacctcaaatgatacgtctgattacaagttgaatgatcaacgccttgctacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                               2489 gaccaaatttataattgggctaactatggtggcgatgatgccttcaatattaagagttcc
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                                  0; Mismatches 244;
      DB 23;
 Score 76.6; DB 23
Pred. No. 1.6e-06;
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1.7%;
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ID AAF26289 standard; DNA; 5340
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                                 265; Conservative
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                Similarity
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                                            This invention describes novel antisense oligonucleotides (I) for inhibiting human egg expression which comprise a sequence corresponding to a nucleotide sequence encoding a defined part of a human eg5 or its mutated form to give increased binding affinity. The invention also describes (I) production of (I) by condensing monomers in a solid phase; (2) use of (I) to prevent the expression of human eg5; and (3) an inhibition process using (I).
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                                                                                                                                                                                                                          NOTE: This sequence is represented as SEQ ID 20 in the SEQ ID list but as SEQ ID 21 in the body of the specification.
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Pred. No. 3.2e-06;
0; Mismatches 310; Indels
                                                                                                                                                                                                                                                                                                   Sequence 5340 BP; 1613 A; 675 C; 466 G; 2586 T; 0 other;
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Best Local Similarity 45.8%;
Matches 262; Conservative
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as (II) and sites expressing (III). (I) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in classonsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197 AAS94564 represent novel human classons contains an expensible disorders of the invention.

Note: The sequence of this patent did not appear in the printed contains as obtained in electronic format directly from WIPO
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1.6%; Score 75.6; DB 23;
Best Local Similarity 50.6%; Pred. No. 3.6e-06;
Matches 267; Conservative 0; Mismatches 249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 25771; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT;
                                                                                                                                                                                                                                 2000US-0540217
2000US-0649167
                                                                                                                                                    30-MAR-2001; 2001WO-US08631
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                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
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WO200175067-A2
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) as useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensizes, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on bNA and amino acid sequences. AAS64197-AAS94564 represent novel human
                                           3521
                                                                                  2541
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                                                                                                                                                                                               3582 agaaagccagaagcttcagcagagcgctaaaaaacgcga---tgctgagttagcgaacgg 3638
        2481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                      2425 agaaaatggtgatcgttatcttgtattcgaagctaatactgggacagaa---gattacca
                                                                                                    2482 aagtgacgaccaaatttataattgggctaactatggtggcgatgatgccttcaatattaa
                                                                                                                                                        2542 gagttccttcaagcttttgaataataagaaggatcgtgaattggctggtttagctaatgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodyversity
                                                                                                                                                                                                                                                          3639 cgccctcggtatcatagagttaaataatgattacacattgaaaaaagt 3686
                                                                                                                                                                                                                                      2602 tgcacttggtatcttaaagctcactaacaatcaaagtaagccaaaggt 2649
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                                                                                                                                                                                                                                                                                                                                                                             BP.
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23-AUG-2000; 2000US-0649167.
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           Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                      2125 taaagaaacaaatgtgttccaagaatggtcaggttcagctattgtaaatgatgatgtac 2184
                                                                                                                                                                                                                                                                                                                                                3282 gacaacagcgcaggtaaatgtgtcaaaatctgatgacacactcaaaatcaacggagtgga 3341
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                                                                                                                                                                                                                    3168 tcaatatggagatcagacgcaagaatggtccggttctgcaacctttacatctgacggaaa
                                                                                                                                                                                                                                                                              3228 aatccgtttattctacac----tgactattccggtaaacattacggcaaacaaagcct
                                                                                                                                                                                                                                                                                                                                                                            2305 taattatcaagttttgtttgaaggtgatggatttcactaccaaacttatgaacaattcgc
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                                                                            Sequence 3990 BP; 1165 A; 971 C; 893 G; 961 T; 0 other;
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                                                                                                                         Query Match
1.6%; Score 75.6; DB 23;
Best Local Similarity 50.6%; Pred. No. 3.6e-06;
Matches 267; Conservative 0; Mismatches 249;
diagnostic coding sequences of the invention.
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23-AUG-2000;
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The invention tradecs to isolated purjunctaclibe (i) and purpertide (II) sequences. (I) is useful as hybridisation probes, only peptide (II) sequences. (I) is useful as hybridisation probes, only gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The color identifying expressed genes. (I) is useful in gene therapy techniques for identifying expressed genes. (I) is useful in gene therapy techniques (I) restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as for a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. (I mapping of sites expressing trother traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostics, forensics, gene mapping, identification of mutations cand to produce other types of data and products dependent on DNA and diagnostic coding sequences of the invention.

Camino acid sequences AsSG4197-ASS4564 represent novel human of diagnostic coding sequences of the invention.

Consistent of the printed of the printed consistent of the printed consistent of the printed of sequences of the invention of the printed of the format directly from WIPO
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                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                            invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.6%; Score 75.6; DB 23;
50.4%; Pred. No. 4e-06;
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                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 21643; 103pp; English.
                                                   Tang YT;
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                                                 Drmanac RT, Liu C,
                                                                                          2001-639362/73
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P-PSDB; ABG21652
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Matches 269; (
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques of cridentifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. (I) end (II) are useful for treating creating treating applymential and polynucleotide sequences have applications in cresponsible for genetic disorders or other traits to assess biodiversity amino acid sequences. AAS64197-AAS94564 represent novel human coid sequences of the invention.

Condition of the printed coding sequences of the invention.

Condition of the printed coding sequences of the invention.

Condition of the printed coding sequences of the invention.

Condition of the printed coding sequences of the invention of condition of coding sequence data for this patent did not appear in the printed consequence.
5484 ccgtaaagaaagccagaagcttcagcagagcgctaaaaaacgcga---tgctgagttagc 5540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                     2596 taatggtgcacttggtatcttaaagctcactaacaatcaaagtaagccaaagt
                                                            Sequence 1866 BP; 581 A; 428 C; 436 G; 420 T; 1 other;
                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #21818.
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2000US-0649167.
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P-PSDB; ABG21827.
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23-AUG-2000;
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Length 1866;

1.6%; Score 75.4; DB 23; 50.7%; Pred. No. 3.3e-06; 11ve 0; Mismatches 246;

Similarity 50.7 55; Conservative

Query Match Best Local Simil Matches 265; (

ttaccaaagtgacgaccaaatttataattgggctaactatggtggcgatgatgcttcaa 2535

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5424 ataccaaggcgaagaatctttatttaacaaagcgtactacggcggcggcacgaacttctt

2536 tattaagagttccttcaagcttttgaataataagaaggatcgtgaattggctggtttagc 2595 .

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Page 11

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2251
2132 acaaatgtgttccaagaatggtcaggttcagctattgtaaatgatgatggtacaattcaa 2191
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                265 ttattctacac----tgactattccggtaaacattacggcaaacaaagcctgacgaca 318
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## AAS87349 standard; cDNA; 1866 (first entry) 13-FEB-2002 AAS87349; RESULT 14 AAS87349

DNA encoding novel human diagnostic protein #23153.

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

Homo sapiens

WO200175067-A2.

11-OCT-2001

30-MAR-2001; 2001WO-US08631

31-MAR-2000; 2000US-0540217 2000US-0649167 23-AUG-2000;

(HYSE-) HYSEQ INC.

Drmanac RT,' Liu C,

Tang YT;

2001-639362/73. P-PSDB; ABG23162

AAS86020 standard; cDNA; 1032 BP

RESULT 15 AAS86020

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodiversity

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome configures are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (I) crestore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as imaging of sites expressing (II). (I) are useful in medical disorders involving aberrant protein expression or biological activity. (IT) and its binding partners are useful in medical disorders involving aberrant protein expression or biological activity. (I cresponsible for genetic disorders or other traits to assess biodiversity amino acid sequences. AAS64197-AAS94564 represent novel human cold sequence data for this patent did not appear in the printed consisting the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
                    SEQ ID No 23153; 103pp; English.
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Sequence 1866 BP; 581 A; 428 C; 436 G; 420 T; 1 other;

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2371
                                                             2132 acaaatgtgttccaagaatggtcaggttcagctattgtaaatgatgatggtacaattcaa 2191
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Query Match 1.6%; Score 75.4; DB 23; Best Local Similarity 50.7%; Pred. No. 3.3e-06; Matches 265; Conservative 0; Mismatches 246;
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2372 aaagatcgtgaaaatgatgattactgcttacgtgacccacacgttgttcaattagaaaat

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820 cagaagettcagcagagegetaaaaaaegegga---tgetgagttagegaaeggegeeete 876

ggtatcttaaagctcactaacaatcaaagtaagccaaaggt 2649 

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polymerase chain reaction (PCR) primers, allogomers, and for chromosome and gene mapphing, and in recombinant production of (II). The and gene mapphing, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapphing, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and not produce other types of data and products dependent on DNA and diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed setting in the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the minner of the m
                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                        DNA encoding novel human diagnostic protein #21824.
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                                                     (first entry)
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P-PSDB; ABG21833
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AAS86020;
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Search completed: September 22, 2002, 09:39:30 Job time: 28064 sec

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Gaps

0; Mismatches 245; Indels 12;

1.6%; Score 75; DB 23; Length 1032; 50.7%; Pred. No. 3.4e-06;

Best Local Similarity 50.77 Matches 264; Conservative

Query Match

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406 aaagatcagaacgcaagaatggtccggttctgcaacctttacatctgacggaaaaatccgt 465

2192 ctattttcacctcaaatgatacgtctgattacaagttgaatgatcaacgccttgctacc 2251

466 ttattctacac----tgactattccggtaaacattacggcaaacaaagcctgacaaca 519

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AE201315 Dugesia p
AE002745 Drosophil
ACO10211 Drosophil
ACO10211 Drosophil
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AE04539 Staphyloc
AE010124 Staphyloc
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X022404 Oryza sat
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X0225 Trypanosoma
AF001520 Bacillus
AF001519 Bacillus
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AF001519 Bacillus
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AF104350 Dictyoste
ACO10481 Drosophil
AF104350 Dictyoste
ACO10818 Drosophil
AF104350 Dictyoste
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Lactobacillus reuteri
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
Lactobacillus.
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AX316615 Sequence
AX316616 Sequence
M18954 S.mutans fr
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Patent: WO 0190319-A 10 29-NOV-2001;
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AX316622
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Score

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25 Others
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Lactobacillus.
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van Geel-Schutten,G.H., Rahaoui,H., Dijkhuizen,L. and
Hijum,S.A.
Novel fructosyltransferases
Patent: WO 0190319-A 3 29-NOV-2001;
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Pred. No. 3.4e-99;
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AX316615
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aggttcaatctttggaactaaagaaacaaatgtgttccaagaatggtcaggttcagctat
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Lactobacillus reuteri.
Lactobacillus reuteri
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
Lactobacillus.
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CCCCGTTGCCGGAAAAGATGACCAAGTATTAGTTACTTCATATATGACTAATAGAAATGG 1871
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/note*"Putative expression-regulating region"
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    /note="Putative expression-regulating

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Pred. No. 3.4e-99;
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/organism="Lactobacillus reuteri"
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van Geel-Schutten,G.H., Rahaoui,H.,
Hijum,S.A.
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Patent: WO 0190319-A 4 29-NOV-2001;
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Sequence 4 from Patent W00190319.
Ax316616
Ax316616.1 GI:17899730
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Best Local Similarity 59.0%;
Matches 1266; Conservative
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                                                             CGCATTTAATATCAAGAGCTTATTTAGAATTCTTTCCAATGATGATATTAAGAGTCGGGC
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SSELAERSOVGENTTASSSAAENOAKTEVOETPSNAPAATVENTOGTTKY ITDNAAV
ESKASKTKDOAATVTKTAASTPEVGGTONEKDEKAKTREADITTPRNTIDEYGLTGOAR
KIATERGINLSSLTGOKOVELINKVKLTSDAQTGHOWTYCEPKIAOTTLIAODERYAIP
YFNAKAIKNKAATTRDAQTGQIADLOWDSWPVQDAKTGEVINNNGYQLVVAMMGIP
NTDNIHIYLLYLNKYGDNNFDHWKNAGSIFGY VERTPLTGWENGSATVNRGDSLOKLYTY
VTSDKNSNNORLAATVNIGFDDQDVRILGFEDOTVALTEGVWAYHYGSYQQMRSTF
TGADNIAMRDPHYIEDENGDRYLLYFEASTGTENYGGEDQIYFTTNGGSSAYNVKSLF
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SDKYYLFTASRLNIGSNNDAWNKANEVYGDNYVMLGYVSDQLTNGYKPLNNSGYVLTA
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KRYPYRYEKLSAGTGSYFGGGREDTVFYDELIDHDFASNIFGDSMEPIFLNGEVAL
IKQTGFDYDGAIYALDWDGQTYIKKVYREFGGLRLVSLNKKYADKFAPYDENPHIGL
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                            Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                                                        fructosyltransferase
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/product="fructosyltransferase"
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gene and flanking regions
J. Bacteriol. 170 (2), 810-816 (1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone-"pSS22 and pTS102.
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/note="ORF3; putative"
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/note="ORF2; putative"
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                                                      Streptococcus.
1 (bases 1 to 4305)
Shiroza,T. and Kuramitsu,H.K.
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/note="putative"
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      Length 4305;
  Score 562; DB 1; Length 43
Pred. No. 2e-86;
0; Mismatches 866; Indels
  12.1%;
Query Match 12.17
Best Local Similarity 56.67
Matches 1168; Conservative
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BCT 12-FEB-2001 gene, complete IS1161

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TASSEAADTHTEVDLKVSENSAANANLSKLNGRIKSIVEENNTSSDIVTFEERIAL
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DWINDKSSESLVHVGDQNSAKLPNEDFNVDYYAVSGYGLKPHTYPTVDGSTGVSEAHG
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                                                                                                                                      1 (bases 1 to 3600)
Rathsam,C., Giffard,P.M. and Jacques,N.A.
The cell-bound fructosyltransferase of Streptococcus salivarius:
the carboxyl terminus specifies attachment in a Streptococcus
                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 3600)
Jacques, N.A.
Direct Submission
Submitted (04-JAN-1993) Institute of Dental Research, Australia
Location/Qualifiers
1. 3600
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                                                                    STRFTFB 3600 bp DNA linear Streptococcus salivarius fructosyltransferase (ftf) cds; uracil phosphoribosyltransferase gene, 5' end; transposase gene, 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Streptococcus salivarius"
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220. 3129
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/gene-"ftf"
/gene-"ftf"
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J. Bacteriol. 175 (14), 4520-4527 (1993)
93322332
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Streptococcus salivarius
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/note="ORF2; putative"
/codon_start=1
/trans_trable=11
/product="uracil phosphoribosyltransferase"
/protein_id="AAA71926.2"
/db_xref="GT:12597937"
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SRDLPLEEVETOPFTYTVQKQLSGKKLAIVPILRAGIGMVDGFLSLVPAARVGHIGM
YRDEETLEPVEYLVKLPEDIDQRQI"
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                                                                                                                                      Match 9.9%; Score 459.2; DB 1; Local Similarity 58.1%; Pred. No. 7e-69; les 950; Conservative 0; Mismatches 624;
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                                                                       GAGATGACGCTTTAACCTTAAGTCATTCCTCAATATTGTTAATAATAAACACCTTTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1796 ATCCATCTGTAGCTGAACTTTACACACCGCTTGTCACTAGCCATGTTACTGATGAG
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                                                                                                                                                                       gcgatgatgccttcaatattaagagttccttcaagcttttgaataataagaaggatcgtg
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                                                 tacgtgacccacacgttgttcaattagaaaatggtgatcgttatcttgtattcgaagcta
                                                                                                                                              atactgggacagaagattaccaaagtgacgaccaaatttataattgggctaactatggtg
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Lactobacillus casei.
Lactobacillus casei
Bacteria, Firmicutes, Bacillus
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AJ003194.1 GI:2673746
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AF012532 Bacillus subtilis strain 168 trp02 YefA (yeefA) gene, partial cds, and YefB (yefB), YefC (yeeA (yeeA), YeeB (yeeD), YeeC (yeeC), YeeB (yeeF) genes, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (03-JUL-1997) Borriss R., Humboldt University, Institute
of Biology, Chausseestrasse 117, Berlin, Germany, D-10115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus subtilis.

Bacillus subtilis

Bacteria, Firmicutes; Bacillus/Clostridium group;

Bacteria, Firmicutes; Bacillus/Clostridium group;

Bacillus/Staphylococcus group; Bacillus.

1 (bases 15361 to 18622)

Henriques, A.O., Beall, B.W., Roland, K. and Moran, C.P. Jr.

Henriques, A.O., Beall, B.W., Roland, R. as 19ma E-controlled operon affecting polypeptide composition of the coat of Bacillus subtilis spores J. Bacteriol. 177 (12), 3394-3406 (1995)
                                               1503 ACGTCCTGTTCTGTATAATTATCAATATCTGTTCGCTTTGGAATTATTTCCCGGATTAAT 1562
                                                                                                                                                                                                                                                                                                                                                                 gotactcctaaacgtcctcgaatatcattcaagccaagaaattcacgcccatgatctgga 4082
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/gene="yefA"
/note="similar to E.coli hypothetical RNA
methyltransferase: SwissProt Accession Number P55135;</pre>
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Borriss,R. and Schroeter,R.
The 55-58 degree segment of the Bacillus subtilis chromosome, region spanning from the purA gene cluster to the cotJ operon Unpublished
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/organism="Bacillus subtilis"
            Mismatches
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          278;
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ENDVRRAVARGLASKTTTYTVGVILEPUTNESSLARGIDDVATNKYN NILLANSD
ENNOKEVTVLATLLEKGVDGLIFMGHELTDSTRAFESRSKTPVVLAGSIDPDEGVGSV
NIDYVAAVEEATRQLLESGNKRVALATGSLTHPINGOFRLKGYRQALEKAGVAYDESL
NTENBENSYGGTALFPKLQKVGATAVTAGDDELAVGLLDGALDKGYRCPDDFEIITSN
NTKLTEMTRPQLTSIDOPLXDIGAVARLLTKMMNKEBIEEKTVMLGFDILKRGSTK"
1346. 1391
Gpen="Copp"
Complement(1403. 2389)
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/transl_table=11
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/protein_id="CAMO5973.1"
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/db_xref="STREMBL:050356"
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//traslation="regstyte; proprings a sprupes sognoog t sedankmam
pottgiegsngdriggiggigtitefffthegepty the papt a sprupes sognoog t sedank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HQWOVSYNTIYRHIYQHNLGEKYSSRGDTGIQRHLRHKHTRHSKNTRHREVQTDYI
SHERPEFINDRQRIGDWEIDYVIGKTGHSILLTVVDRLSKTTLIKKVQKDSQEINK
SLVELLGAIPKEFVHSITPDHGTEETHLDEISERLGYTVYWDDPYSPEORGTNENTNG
LIRBIIPKRTDIDNYTEQDVEHÇQKQLNQRPRKVLNYETPYEVFFDKPLHLV
          de la Coma
                                                                                    mediated
Agroquimica y Tecnologia de Alimentos (CSIC), Poligono de s/n PO. Box 73, 46100 Burjassot, Valencia, 46100, SPAIN 2 (bases 1 to 3018) Monedero, W., Gosalbes, M.J. and Perez-Martinez, G. Catabolite repression in Lactobacillus casei ATCC 393 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221.6; DB 1; Length 3018;
No. 2.5e-28;
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                                                                                              by CcpA
J. Bacteriol. 179 (21), 6657-6664 (1997)
98012962
                                                                                                                                                                              1. .3018
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                                                                                                                                                            Location/Qualifiers
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237. .242
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284. .290
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ELSTRRKNEIEEAILEILDLREEQGGTLAELYNPSTMPIELKVAHEKLDGIVERAYRQ
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VRQHVVLDTVMKGAKSEVVGSKEFIRMADKFINIEDLDINLIDSINPFQKAFEVLSKE
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KISSIDDILKSGLSALLGDNLNNDITRSIFDTSSLQKVTTMPEYVAKRKIKDFGKFE
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PQISSIKNLYKIGFTTGSVENRIRNAENQSTYLYAPVEIVTTYQVFNNNASKFETAIH
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/note="rho
                                                                                                                                             /gene="ye
4171. 50
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similar to Chlamydia trachomatis Homl: SwissProt Accession
Number P55137"
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AINITNEDISNFETTLHQLSKDLEFQKIEKEIIDFKKSLDKFMKEGTLTPEMLHLLVD
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NIIETNRGLDLFLIRLECFFAEDTDIFKRNSTYNLKTLTEEDGSNINKLFADLFIY
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GSMIQAVASEESRSYLGMHYTSVPNIMKVIKPLFLDKLNQSFLDAYDDYTKLENLLTR
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OERISISKNHREKSTDKGTNKLALTPWKFRDTHETTNYSIVVBSVSSENRFYIPWGLA
GADTILSNLIYVIYDAEIXLLGILMSRMHMTWVKAVAGRLKTDYRYSAGLCYNTFPIP
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1024. .1030
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1505. .1512
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1520. .4159
                                                                                                                                                                                                                                                                    'gene="yefB
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⁄qene="yeeA
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gene

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RBS

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OYAQTNAGKPODRKPDDDGGHLIATQFKGSGQFDNIVPMNSQINRSGGKWYEMEQEWA
KALSKKPPKKVAVQIEPVYSGDSLRBSYFDVTYRIGSRKEISVSIKISLGYRRMETRK
MQDLYQLIGEKLNDIIPGEWTKIYLYAEVLDDSTWVLFHFRTPENNQIIYSQDIPSHY
NVSROIFKTLIRELRELFEERTEHRNNNDDVWTNLTLTLDRSGEFQLDYNYDDILAS
ELDGYERIAIWEYKNIGILPEDEDDKEFVISYLGL
                                                                                                                                                                   /note="similar to Bacillus subtilis orf94 hypothetical
59.7 kDA protein in CWLA-CISA intergenic region: SwissProt
Accession Number P45942"
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                                                                                                                                                                                                                                                                                                                                                                                                            ttaacctcgcaggagagaaaagaagcaattagtaaggatccatatgcagataaatttatt
                                                                                                                                                                                                                                                                                                                                                                                                                            aggocttatttaggtgctaaaaatttcattcatggaactgctaggtactgtatttggtta
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                                                                                                                                                                                                                                2.9%; Score 136; DB 1; Length 18622; 48.6%; Pred. No. 7.3e-14;
                                                                                                                                                                                                                                               Pred. No. 7.3e-14;
2; Mismatches 477; Indels
                                                                                            /gene="yeeE"
complement(9541. .10791)
                                                                                                                       /gene="yeer"
complement(9541. 10791)
                                                                              complement(9464. .9470)
                                                                                                                                                        /gene="yeeF"
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                             Similarity
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Bacterla; Firmicutes; Bacillus/Clostridium group;
Bactillus/Staphylococcus group; Bacillus.

El (bases 1 to 213109)

RKUNStf.; Ogasawara,N. Moszer,I., Albertini,A.M., Alloni,G., Azevedo,V., Bertero,M.G., Bessieres,P., Bolotin,A., Borchert,S., Boursier,L., Brans,A., Braun,M., Brignell,S.C., Boursier,L., Brans,A., Braun,M., Brignell,S.C., Boursier,E., Bruschi,C.V., Caldwell,B. Capuano;V., Carter,N.M. Choi,S.K., Codani,J.J., Connerton,I.F., Cummings,N.J., Daniel,R.A., Denizot,F., Devlae,K.M., Dusterhoft,A., Ehrlich,S.D., Emmerson,P.T., Entian,K.D., Errington,J., Pabret,C., Ferrari,E. Foulger,D., Fritz,C., Fujlta,M., Fujlta,Y., Fuma,S., Galizzi,A., Galleron,N., Ghim,S.Y., Gaser,P., Goffeau,A., Golightly,E.J., Galneot,D., Hand,S., Galizzi,A., Handut,A., Hilbert,H., Holsappel,S., Hosono,S., Hullo,M.F., Itaya,M., Jones,L., Joris,B. Karamata,D., Kasahara,Y., Khaerr Blanchard,M., Klein,C., Kobayashi,Y., Koetter,P., Koningstein,G., Lauber,J., Lazarevic,V., Lee,S.M., Lapidus,A., Liu,H., Masuda,S., Kuumno,M., Woltia,K., Lapidus,R., Liu,H., Masuda,S., Mauel,C., Medina,N., Mellado,R.P., Pull,P., Porvollik,S., Prescott,A.M., Persecan,E., Pujic,P., Purnelle,D., Porwollik,S., Prescott,A.M., Persecan,E., Pujic,P., Purnelle,D., Porwollik,S., Prescott,A.M., Parro,V., Pohl,T.M., Purnelle,D., Porvollik,S., Schroeter,R., Scoffone,F., Scklguchi,J., Scrotk,B., Raven,M., Sadale,Y., Sator,S., Schleich,S., Schoeler,R., Schleich,S., Schoeler,R., Schoeler,F., Vasamoto,H., Takaman,K., Tarakashi,H., Takaman,K., Tarakashi,A., Taranesoshi,A., Tanaka,H., Wedler,R., Wanner,F., Vasamoto,K., Yanamoto,H., Wanner,F., Vashikawa,H. and Danchin,A., Wannet,R., Woshikawa,H. and Danchin,A., Tanaka,H.F., Zumstein,E., Yoshikawa,H. and
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Bacillus subtilis complete genome (section 4 of 21): from 600701 to
813890.
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4046 CATGAAAAGTTGGATGGAATTGTAGAAAGAGCGTATCGTCAAAAACAATTTGAATCTGAT 4105
                                                                                              955 ctttgtaaaaccaatattttataaagacagtaaatgttaatttgataaaaacatattt 1014
                                                                                                                                                                                                                         The complete genome sequence of the gram-positive bacterium
                                                          895 caagaaatcgtagaacatctatttaagatgtatgaaaaactgactaaaggtgaaagataa
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Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.
Direct Submission
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Nature 390 (6657), 249-256 (1997)
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Z99107.1 GI:2632866
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1. .213190 /organism="Bacillus subtillis"

source

us-09-995-587a-10.rge

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KGLAQLALQTLDERARELGAERLAHVFAHNETAVYLYQKMGYAMTNIRMRKQLC"
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ALKIVIALIALIYGLYMIRKGFSTSSGVSSFTWINKGHGGLFPNGMIGFILSFOWVY
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PFVQVFVAVGIVGAASIINFVVLTSAASACNSAVFSTSRMYYSLAKDHNAPESMAKLT
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IHFAGPSILFAXMITGIICFLIMRSLGELLLSNLNYHSFVDFVQDYLGDMAFITGWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to hypothetical proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 136; DB 1;
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complement(5428. .7089)
/gene="ydgF"
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IAVNOEGRLPIELIHDSEIIENNLKQNRLTESWLEBELRKRDIKVKETVYAVLLGNGD
IYVDQYKDHISVPMDKE"
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ERIIQLPEAAETHLLQIQLLNGLLHISYPRQVETVAFNKGL"
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TESFLLIGIKDPASLAAEVVNLLIYCMLPKCNDVR"
join(2610: .2954,3074: .3091)
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/note="similar to hypothetical proteins from B. subtilis"
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complement(1199. 1441)
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                            /db_xref="taxon:1423"
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               19;
               Indels
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2; Mismatches 477;
Best Local Similarity 48.6%
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L Submitted (28-JUN-1999) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA On Jul 17, 2001 this sequence version replaced gi:12746529.

* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.
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El-Sayed, N.M., Ghedin, E., Song, J., Larkin, C., Wanless, D., Jones, K., Et-Sayed, N.M., Ghedin, E., Zhao, H., Mason, T., Militscher, J., Pai, G., Van Aken, S., Utterback, T., Khalak, H.G., Gerard, C., Leech, V., Ullu, E., Melville, S., White, O., Adams, M.D., Donelson, J.E. and Fraser, C.M. Trypanosoma brucei GUTatl0.1 RPC193-3415 BAC genomic sequence
                                        SEQUENCING
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llarity 49.8%; Pred. No. 3.8e-12;
Conservative 0; Mismatches 320
                AC007926 155204 bp DNA
Trypanosoma brucei chromosome II clone
IN PROGRESS ***, 1 ordered pieces.
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El-Sayed, N.M., Khalak, H. and Adams, M.D.
Direct Submission
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SEQUENCING IN PROGRESS ***, 1 ordered pieces.
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El-Sayed, N.M., Ghedin, E., Song, J., Larkin, C., Wanless, D., Jones, K., Peterson, J., Hou, L., Zhao, H., Mason, T., Miltscher, J., Pai, G., Van Aken, S., Utterback, T., Khalak, H.G., Gerard, C., Leech, V., Ullu, E., Melville, S., White, O., Adams, M.D., Donelson, J. E. and Fraser, C. M. Trypanosoma brucei GUTatlo. I RPCI93-1118 BAC genomic sequence
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Submitted (30-0CT-2000) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA.

**NOTE: This is a 'working draft' sequence. It currently **Consists of I contigs. Gaps between the contigs. are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between the contigs.

**Is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have this sequence will be replaced
                                                                                             aacagatgatcaaattaatgaattaaataagattaacttctctaagtctgctgaaaaggg
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1 171798: contig of 171798 bp in length.
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ilarity 51.1%; Pred. No. 2.3e-08;
Conservative 0; Mismatches 232;
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1-Sayed, N.M., Khalak, H. and Adams, M.D.
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1 (bases 1 to 155204)
El-Sayed,N.M., Ghedin,E., Song,J., Larkin,C., Wanless,D., Jones,K.,
El-Sayed,N.M., Ghedin,E., Zhao,H., Mason,T., Militscher,J., Pai,G., Van
Aken,S., Utterback,T., Khalak,H.G., Gerard,C., Leech,V., Ullu,E.,
Melville,S., White,O., Adams,M.D., Donelson,J.E. and Fraser,C.M.
Trypanosoma brucei GUTatl0.1 RPCI93-3H15 BAC genomic sequence
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Submitted (28-JUN-1999) The Institute for Genomic Research, 9717
Medical Center Dr. Rockville, MD 20850, USA
On Jul 17, 2001 this sequence version replaced gi:12746529.
* NOTE: This is a 'working draft' sequence. It currently consists of I configs. Gaps between the configs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
* This sequence will be replaced show the finished sequence as soon as it is available and the accession number will be preserved.

* This Sequence as soon as it is available and the accession number will be preserved.
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El-Sayed, N.M., Khalak, H. and Adams, M.D.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STH278471 36272 bp DNA linear BCT 04-SEP-2001 Streptococcus thermophilus partial site-specific integrative conjugative element ICESt1 and flanking regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AJ278471.1 GI:15485427
repetitive sequence; stem loop.
Streptococcus thermophilus.
Streptococcus thermophilus
Streptococcus thermophilus
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus.

1 (bases 1 to 36272)
Guedon,G., Bourgoin,F., Pebay,M., Roussel,Y., Colmin,C.,
Simonet,J.M. and Decaris,B.
Characterization and distribution of two insertion sequences,
IS1191 and iso-IS981, in Streptococcus thermophilus: does
intergeneric transfer of insertion sequences occur in lactic acid
                                                                                                                                           tgccggtagtttaacagatgatcaaattaatgaattaaataagattaacttctctaagtc 1764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       three Streptococcus
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                                                                                                                                                                                                                                  tgctgttgttaatgaaagcaaaaatactaacaatactgaaaatgctgttgttaatgaaaa 1524
                                                                                                                                                                                                                                                                                        1525 caaaaatactaacaatactgaaaatgctgttgttaatgaaaacaaaaatactaacaacac 1584
                                                                                                                                                                                                                                                                                                                                                 1585 agaaaacgataatagtcaattaaagttaactaataatgaacaaccatcagccgctactca 1644
                                                                                                               1345 taatactgaacgtcaagctaatggtcaaattggcgtagatggaaaaattattagtgctaa 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1765 tgctgaaaagggtgcaaaattgacctttaaggacttagaggggattggtaatgctattgt 1824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 36272)
Roussel,Y., Bourgoin,F., Guedon,G., Pebay,M. and Decaris,B.
Analysis of the genetic polymorphism between three Streptococthermophilus strains by comparing their physical and genetic organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microbiology (Reading, England) 143 (Pt 4), 1335-1343 (1997)
97286550
                                                                                                                                                                                                                                                                                                                                                                                                          1645 agcaaacttgaagaagctaaatcctcaagctgctaaggctgttcaaaatgccaagattga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53986 TATATACTAATATATAATAAGAGCAGTAATAATAATGATAATGATAATGATAATAG
                                                                 Length 155204;
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                                                                                             Indels
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95379495
                                                                                            242;
                                                              ; DB 2
.5e-08;
                                                                                          Mismatches
      42525
                                                             Score 101.8;
Pred. No. 3.5
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Direct Submission
Submitted (16-JUN-2000) Burrus V., Universite Henri Poincare (Nancy
1), Laboratolize de Genetique et Microbiologie - UA INRA 952,
Laboratolize de Genetique et Microbiologie - UA INRA 952,
Faculte des Sciences - BP 239, Vandoeuvre-les-Nancy 54506, FRANCE
Overlapping sequences: the left terminus of ICESt1 (AJ243105), the
IIGST1 (AJ271594) and a region including IS1191 and IS981 (X71808)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="varIC region"
/clone="b40"
/note="integrative conjugative element ICESt1 and flanking
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                                                                                       Applied and environmental microbiology. 66 (4), 1749-1753 (2000) 20208895
                                                          ICESt1, in the
                                                                                                                                                                                                                                                                  5 (bases I to 36272)
Burrus, V., Bontemps, C., Decaris, B. and Guedon, G.
Characterization of a novel type II restriction-modification
System, Sth3681, encoded by the integrative element ICESt1 of
Streptococcus thermophilus CNR2368
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214. .219
/evidence=not_experimental
                                                                                                                                                                                                       of
                                                                                                                                            4 (bases 1 to 36272)
Burrus, V., Pavlovic, G., Decaris, B. and Guedon, G.
Modular structure of the integrative element ICEStl
Streptococcus thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1257. 1287 // Anote="R5 inverted repeat, probable bidirecrino-independent transcriptional terminator
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/note="attL attachment site"
1432. .1445
/rpt_family="R7 imperfect inverted repeat"
3 (bases 1 to 36272)
Burrus, V., Roussel, Y., Decaris, B. and Guedon, G.
Characterization of a novel integrative element,
lactic acid bacterium Streptococcus thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. 36272
//organism="Streptococcus thermophilus"
/strain="CNR2368"
/db_xref="taxon:1308"
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/note-"Integrative Conjugative
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/function="core sequence of
/rpt_family="R1"
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/evidence=not_experimental
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/note="EE132.3 region"
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/note="outward facing"
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1290. .36049
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/note="IS1195L"
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Protein_id="Cac67523.1"

db_xref="G1:15485429"

/tanslation="MNYYNKYSICLQMISAVIIGTIFGSLLPOFSSIYOFLGRAF

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ISCLVSWYILPUVFPYTVLXVBATELINKESLGKLILKSTLYFFIITTIITGIFVTGSYLL

ISCLVSWYILFYTITALHYVVPAIYKYVELIKKYPETGYFGFIASDVATTGFEKLISL

GEFVIGTYVAXSILAHFFYPLLAYIFELNYFOLIKSIWNLLLAFISGSSSVVLPFLL

RRLKNNGSDENITDLVVPLGYTFNLQGAAVYFSIATIYIVNYVNINISTSQIIYTIFI

LELIGRTAATVPSGAIVVLLASATMLGLPKEGVALIFAVDFFVNAGRTALNVLGGGMT
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*** SEQUENCING
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1 (bases 1 to 133075)
El-Sayed,N.M., Ghedin,E., Song,J., Larkin,C., Wanless,D., Jones,K.,
Peterson,J., Hou,L., Zhao,H., Mason,T., Militscher,J., Pal,G., Van
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                                                                                                                                                                                       /transl_table=11
/evidence=not_experimental
/product="putative glutamate/aspartate-proton symport
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 36272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 98.4; DB 1; Length 36
57.0%; Pred. No. 1.7e-07;
Live 0; Mismatches 136; Indels
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4728. .5657
/note="orfx
                                                                                                       /evidence=not_experimental
3491, 4708
                    /rpt_type=DIRECT
3479. .4708
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4715. 4722
/note="orfx"
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                                                                        3479. .3486
/gene="gst"
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/gene="gst"
                                                     /gene="gst
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BCHEIDVLITINDIHTPYFTTEDYTSKKDIQFKYVLKONIYTRINDIHTPYFTSTTTTV
EGHEIDVLITINDIHTPYFTTEDYTSKKDIQFKYVLKONIYTRINDIHTPINRTAD
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TELKKFVNFLDKNVELLKNDKIFPKLVLDRRYYEMEDFDAIEYVVARKIKWLYENRYLK
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/function="putative phase variation regulation"
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/rpt_family="R8 direct repeat"
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Aken,S., Utterback,T., Khalak,H.G., Gerard,C., Leech,V., Ullu,E., Melville,S., White,O., Adams,M.D., Donelson,J.E. and Fraser,C.M. Trypanosoma brucei GUTatl0.1 RPC193-2809 BAC genomic sequence
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                                                                                                                                             9712
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S El-Sayed, N.M., Khalak, H. and Adams, M.D.

Direct Submission

L Submitted (GB-NOV-2001) The Institute for Genomic Research, 97112

Medical Center Dr., Rockville, MD 20850, USA

On Dec 12, 2001 this sequence version replaced gi:16974132.

* NOTE: This is a "working draft, sequence. It currently

* Consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

is believed to be correct as given, however the sizes

of the gaps between them are based on estimates that have

This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
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Anopheles gambiae putative odorant receptor Or2 gene, complete
AF364131
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Anopheles.
1 (bases 1 to 4865)
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Pred. No. 1.4e-07;
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26639 c 28358 g 32609
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Matches 195; Conservative
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REFERENCE

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join(<455. .670,768. .851,948. .1372,1571. .1670,1753. .1854,
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join(455. .670,768. .851,948. .1372,1571. .1670,1753. .1854,
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                                                                                                           2 (bases 1 to 4865)
Pox.A.N. Pitts,R.J., Robertson,H., Carlson,J. and Zwiebel,L.J.
Direct Submission
Submitted (27-MAR-2001) Biological Sciences, Vanderbilt University,
390 24th Ave. S., Nashville, TN 37235, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIRLYSSWGDMSELIINGYFFTULYFNIULRTSFLUINRRKFETFFEGVAAEYALLEKN
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               and Zwiebel, L.J.
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Föx,A.N., Pitts,R.J., Robertson,H.M., Carlson,J.R. and Zwiebel,L. Candidate odorant receptors from the malaria vector mosquito Anopheles gambiae and evidence of down-regulation in response to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1314 aaagtaacaattacaacggtgttgctgaagttaatactgaacgtcaagctaatggtcaaa 1373
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Proc. Natl. Acad. Sci. U.S.A. 98 (25), 14693-14697 (2001)
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Pred. No. 2.8e-07;
0; Mismatches 275; Indels
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Search completed: September 22, 2002, 05:40:23 Job time: 21803 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

September 26, 2002, 18:26:43; Search time 22.4 Seconds (without alignments) 1369.013 Million cell updates/sec

4149 1 MYKVGKNWAVATLVSASILM.....LYAGSLLALFGLAAIEKRHA 792 US-09-995-587A-11 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	11171111111111111111111111111111111111	055242 streptococc	bacilluc		bacillue	Secondary.							plaise dictionacter		OS4443 attaches														_	Q48258 helicobacte	Q53020 r outer mem	es		P15293 lactococcus
SUMMARIES	ID	SACB STRMIT	SACE STRSL	SACB BACAM	SACB_BACSU	SACB_BACST	INVB_ZYMMO	SACB_ZYMMO	SACB_RAHAQ	SACB_PSESG	SACB_PSESH	SACB_ERWAM	SACB ACEDI	KYK1 DICDI	AAC2 DICDI	DEXT STRMII	TAGE DICOI	HPT2 DETRA	CAPA CAPA	CAR SIANO	DEXT CTEDO	Camp Camp	FNBA CTAAL	Ougho Sand	ACA1 DAMEN	HGD3 HAFTN	Marin 1000	VACA_RELPU	ACL_HELFI	ARF_FLAFA	VAC4_HELPY	OMPB_RICPR	YDBA_ECOLI,	OMPA_RICRI	P2P_LACLC
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	Score	1684.5	1586	751.5	746.5	730.5	309	251.5	245	242.5	240.5	236.5	_	190.5	190	185	185	182	179.5	_	178	174	172	171.5	_	167	166	166	164.5	; -	164	5 0	103	162	100.5
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Ouery Match

40.6%; Score 1684.5; DB 1; Length 797;
Best Local Similarity 44.3%; Pred. No. 1.2e-82;
Matches 370; Conservative 126; Mismatches 230; Indels 109; Gaps

1 MYKVGKNWAVATLVSASILMGGVVTAHADQVESNNYNGVAEVNTERQANGQIGVDGKIIS 60 

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61 ANSNTTSGSTNQESSATNNTENAVVNESKNTNNTENAVVNENKNTN-NTENAVV----- 113

052657 rickettsia P52143 escherichia P44969 haemophilus P49331 streptococc P08987 streptococc P1001 streptococc P80544 staphylococc P96989 r outer mem P52081 staphylococ P54674 dictyosteli P34487 caenorhabdi P47134 saccharomyc		tb; PRT; 797 AA.  Created) Last sequence update) Last annotation update) Lest annotation update) 6-fructosyl transferase).	group; Streptococcaceae;	SEQUENCE FROM N.A. STRAIN-GS-5; MEDLINE-80115184; PubMed-2828325; Shiroza T., Kuramitsu H.K.; "Sequence analysis of the Streptococcus mutans fructosyltransferase gene and flanking regions."; J. Bacteriol. 170:810-816(1988)!- CATALYIC ACTIVITY: SUCROSE + (2,6-BETA-D-FRUCTOSYL)(N) = GLUCOSE + (2,6-BETA-D-FRUCTOSYL)(N+1) (OTHER SUGARS CAN ALSO ACT AS FRUCTOSYL ACCEPTORS)!- SUBCELLUAR LOCATION: Secreted!- SIBLIARITY: BELONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES.	This Swiss-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its modified and this statement is not removed. Usage by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).  EMBL, MI8954; AAA86584.1;
OMPA_RICCN YPJA_ECOLI IGAO_HAEIN GTFD_STRMU GTFL_STRMO GTFL_STRDO MRSP_STAAU OMPB_RICTY ATL_STRAU P3KZ_DICDI YMJB_CAEEL	ALIGNMENTS	PRT; 797 AA. ed) sequence update) annotation update) 2.4.1.10) (Beta-D- ictosyl transferase	Bacillus/Clostridium group;	828325; Streptococcus mut "; 1988). CROSE + (2,6-BETA RRUCTOSYL)(N+1) ( ACCEPTORS). Secreted.	This SWISS-PROT entry is copyright. It is produced the petween the Swiss Institute of Bioinformatics and the European Bioinformatics institute. There are no use by non-profit institutions as long as its contemporation and this statement is not removed. Usage by entities requires a license agreement (See http://www.or.send.an.email to license agreement (See http://www.por.send.an.email to license@isb-sib.ch).  EMBL, MI88551; B28551.  FMR: B28551; B28551.  FMR: B28551; B28551; B28551.  Interpro: IPRO03469; Glyco_hydro_68.  Ffans FPO.435; Glyco_hydro_68.  FFANSUCRASE.
3.9 2021 3.9 1569 1 3.8 1462 1 3.8 1462 1 3.8 1597 1 3.8 1637 1 3.8 1637 1 3.8 1645 1 3.8 1858 1 3.8 1858 1 3.8 918 1	ঝ	STANDAF (Rel. 12, (Rel. 37, (Rel. 37, Precursor (Sucrose		SEGUENCE FROM N.A. STRAIN-GS-5; MEDLINE-88115184; PubMed-2828325 Shiroza T., Kuramitsu H.K.; Sequence analysis of the Strept gene and flanking regions."; J. Bacteriol. 170:810-816(1988)! CATALYIT: ACTIVITY: SUCROSE GLUCOSE + (2,6-BETA-D-FRUCTOR ALSO ACT AS FRUCTOSYL ACCEPT -! SUBCELLULAR LOCATION: Secret -! SIMILARITY: BELONGS TO FAMILY.	This SWISS-PROT entry is copyright. It is between the Swiss Institute of Bioinfort the European Bioinformatics Institute.  The European Bioinformatics Institutions as lon modified and this statement is not removentites requires a license agreement (Sorsend an email to license@isb-sib.ch).  EWBL; M18954; AAA88584.1;
34 160.5 35 160 36 160 37 159 38 159 40 159 42 157 43 157 44 156.5		RESULT 1 SACB_STRWU ID SACB_STRWU AC P11701; DT 01-OCT-1989 OT 10-OCT-1989 OT 15-DEC-1998 DE LEVARSUCTASE	fir. Streptococcus mutans. Bacteria; Firmicutes; Streptococcus. NCBL_TaxID=1309;	SEQUENCE FROM N STRAIN-GS-5, MEDLINE-88115184 Shiroza T., Kure Sequence analysi gene and flankir J. Bacteriol. 17 J. CATALYTIC AG GLUCOSE + (2 GLUCOSE + (2 ALSO ACT AS I. SIMILARITY:	This SWISS-PRC between the Surveen the European B use by non-p modified and tentifies required or send an ema contract manager of the SWISS of the S
		RESULT SACB_S ID S AC P DT 0 DT 1 DE L	50000 A	R R R R R R R C C C C C C C C C C C C C	% 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7

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-QENTTA----SSSAAENQAKTEVQETPSTNPAAATVENTDQTTKVITDNAAVESKASK 108
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STRAIN-ATCC 25975;
MEDLINE-9332332; bubmed-8331080;
RAthsam C., Giffard P.M., Jacques N.A.;
"The cell-bound fructosyltransferase of Streptococcus salivarius: tcarboxyl terminus specifies attachment in a Streptococcus gordonii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                            PATYTVDAQTGKMAHLDVWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPTGDNHIYLL
                                                                                                                                                     YNKYGDNDFSHWRNAGSIFGTKETNVFQEWSGSAIVNDDGTIQLFFTSNDTSDYKLNDQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Levansucrase precursor (EC 2.4.1.10) (Beta-D-fructofuranosy)
Lyansferase) (Sucrose 6-fructosyl transferase).
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NCBI_TaxID=1304;
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                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : |: :: | | : :| | | | : :| | : :| | : :| | : :| ETATSVATSEAVESKASSTAVTSSSDATTPSAT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----NNTENAVVNENKNTNNTENDNSQLKLTNNEQPSAATQANLKKLNPQAAKAV-Q 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAKID-AGSLTDDQINELNKINFSKSAEK--GAKLTFKDLEGIGNAIVKQDPQYAIPYSN 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNHIYLLYNKYGDNDFSHWRNAGSIFGTKETNVFQEWSGSAIVNDDGTIQLFFTSNDTSD 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKEIKNMPATYTVDAQTGKMAHLDVWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPTG
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                                                                                                                                                                                                                                                                                                                                                                            90;
Bacteriol. 175:4520-4527(1993).
CATALYTIC ACTIVITY: SUCROSE + (2,6-BETA-D-FRUCTOSYL)(N) educose + (2,6-BETA-D-FRUCTOSYL)(N+1) (OTHER SUGARS CAN ALSO ACT AS FRUCTOSYL) ACCEPTORS).
SUBCELLULAR LOCATION: SECRETED. CELL-WALL BOUND.
SIMILARITY: BELONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                               Length 969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 NSNTTSGSTNQESSATNNTENAV--VNESKNTNNTENAVVNENKNT----
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                                                                                                                                                                                                                                                                                        LEVANSUCRASE.
                                                                                                                                                                                                                                                              wall
                                                                                                                                                                                                                                                                                                                                            38.2%; Score 1586; DB 1;
41.6%; Pred. No. 2.8e-77;
ative 133; Mismatches 266;
                                                                                                                                                                                                                             InterPro; IPR003469; Glyco_hydro_68.
Pfam: PF02435; Glyco_hydro_68; 1.
Transferase: Glycocyltransferase; Signal; Cell
SIGNAL 1 ? POTENIAL.
                                                                                                                                                                                                                                                                                                                                                                         Conservative 133;
                                                                                                                                                                                                                                                                                                   969 AA; 103983 MW;
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Best Local 3
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNEKYQVPQFDQSTIKN-----IESAKG-----LDVWDSWPLQN-ADGTVAEYNGYHVVF 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMMGIPNSPTGDNHIYLLYNKYGDNDFSHWRNAGSIFGTKETNVF-------QEWS 312
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678 MTNGGDWIWDKSSES----LVHVGDQNSAKLPNE-DFNVDYYAVS---GYGLKPH--TY 726
                                      PKIDQPDQQPSGQNTKNVTPGNG-----DKPAGKATP-----DNTNIDPSAQPSGQN 728
                                                               PTVDGSTGVSEAHGVLTVTVKDGKDKKADKPETPVSPTEGNHSVDDKTNKPGTSKPADNN 786
                                                                                        729 TNIDPSAQXSGQNTKNVTP------GNEKQGKNTDAKQLPQTGNKSG 769
                                                                                                                  --- OPSADKEDKPTNPTNPDSPARTPFPYYGDHSNDNNSSNDHHVAVPVKPSTGDSVG 841
                                                                                                                                                                                                                                                                                                                                                                                                 Pang L.B., Lenstra R., Borchert T.V., Vasantha N.; *Isolation and characterization of levansucrase-encoding gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 NIKKIVKQATVLTFTTALLAGGATQAFAKENNQKAY-KETYGVSHITRHDMLQIPKQ--Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 472;
                                                                                                                                                                                                           01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Levansucrase precursor (EC 2.4.1.10) (Beta-D-fructofuranosyl transferase) (Sucrose 6-fructosyl transferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - INDUCTION: BY SUCROSE. - SIMILARITY: BELONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1- CATALYTIC ACTIVITY: SUCROSE + (2,6-BETA-D-FRUCTOSYL)(N) GLUCOSE + (2,6-BETA-D-FRUCTOSYL)(N+1) (OTHER SUGARS CAN ALSO ACT AS FRUCTOSYL ACCEPTORS).
1- SUBCELLULAR LOCATION: Secreted.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472 LEVANSUCRASE.
52859 MW; F38592D272677E7D CRC64;
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38.0%; Pred. No. 3e-33
                                                                                                                                                                                     472 AA
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Pfam; PF02435; Glyco_hydro_68; 1.
Transferase; Glycosyltransferase; Signal.
                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91092506; PubMed-2265762;
                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus amyloliquefaciens.";
Gene 96:89-93(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X52988; CAA37179.1; -.
                                                                                                                                                                                                                                                                                              Bacillus amyloliquefaciens
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Best Local Similarity 38.09
Matches 190; Conservative
                                                                                                                                                                                     STANDARD;
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P21130;
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491 CDEV----XXKLGDKYYLFSVTRVSRGSDRELTAKDNTIVGDNVAMIGYVSDSLMGKYKP
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"Modulation of Bacillus subtilis levansucrase gene expression sucrose and regulation of the steady-state mRNA level by sacU sacO genes.";
J. Bacteriol. 168.380-388(1986).
-: CATALYITIC ACTIVITY: SUCROSE + (2,6-BETA-D-FRUCTOSYL)(N) - (LUCOSE + (2,6-BETA-D-FRUCTOSYL)(N+1) (OTHER SUGARS CAN ALSO ACT AS FRUCTOSYL ACCEPTORS).
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P05655; P7084;
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last noncation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Levansucrase precursor (EC 2.4.1.10) (Beta-D-fructofuranosyl transferase) (Sucrose 6-fructosyl transferase).
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MEDLINE=8417844; PubMed=6424671;
Fouct A., Arnaud M., Klier A., Rapoport G.;
"Characterization of the precursor form of the exocellular levansucrase from Bacillus subtilis.";
Biochem. Biophys. Res. Commun. 119:795-800(1984).
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Bacillus/Staphylococcus group; Bacillus.
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SEQUENCE
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SEQUENCE 1
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                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
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PIR: S07309; S07309.

Subfilist; B610389; sacb.

InterPro; IPR001469; Glyco_hydro_68.

Pfam; PF02435; Glyco_hydro_68, 1.

Transferase; Glycosyltransferase; Signal; Complete proteome.
               -1- SIMILARITY: BELONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES.
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3FBF2F571B41D5B0 CRC64;
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473 AA; 52971 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328 MKPLIASNTVTDEIERANVFKMNGKWYL---STDSRGSQMTI----DGITSNDIYMLGYV 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 ILKDQTQEMSGSATFTSDGKIRLEYT--DFSGKHYGKQTLTTAQVNVSASDSSLNINGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 473;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Levansucrase precursor (EC 2.4.1.10) (Beta-D-fructofuranosy)
Lransferase) (Sucrose 6-fructosyl transferase).
                                                                                                                                                                                                                                                                                                                                                                                                        Li Y., Triccas J.A., Ferenci T.;
"A novel levansucrase-levanse gene cluster in Bacillus
stearothermophilus ArCc12980 ".
Blochim. Blophys. Acta 1353:203-208(1997).
-!- CATALYITC ACTIVITY: SUCROSE + (2,6 BETA-D-FRUCTOSYL)(N)
GLUCOSE + (2,6 -BETA-D-FRUCTOSYL)(N+1)
ALSO ACT AS FRUCTOSYL ACCEPTORS).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR ELOCATION: Secreted.
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                                                                                                                                                                     Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
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35.9%; Pred. No. 3.9e-32;
tive 93; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003469; Glyco_hydro_68.
Pfam; PF02435; Glyco_hydro_68; 1.
Transferase; Glycosyltransferase; Signal.
SIGNAL 1 29 BY SIMILARITY.
                                                                                                                                                                                                       Bacteria, Firmicutes, Bacillus/Clostridium Bacillus/Staphylococcus group, Geobacillus
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MEDLINE-98007870; PubMed-9349714;
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Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473
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SDSLMGKYKPLNNSGVVLTASVPANWRTATYSYYAVPVAGHPDQVLITSYMSNKDFASGE 596
              Kannan R., Mukundan G., Ait-Abdelkader N., Augier-Magro V.,
Baratti J., Gunasekaran P.;
"Molecular cloning and characterization of the extracellular sucrase
gene (sacc) of Zymomonas mobilis.";
Arch. Microbiol. 163:195-204(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ahn J.Y., Kang H.S.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing beta-D-fructofuranoside residues in Deta-D-fructofuranosides.
-!- SIMILARITY: BELONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kyono K., Yanase H., Tonomura K., Kawasaki H., Sakai T.;
**Cloning and characterization of Zymomonas mobilis genes encoding
**Crealiular levansucrase and invertase.";
Biosci. Biotechnol. Biochem. 59:289-293(1995).
                                                                                                                                                                                                                                                                                                                                                                              extracellular
                                                                                                                                                                                                                                                        Zymomonas mobilis.
Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
                                                                                                                                           10VB_2YMMO STANDARD; PRT; 413 AA.
060115; 060117; 060125;
15-DEC-1998 (Rel. 37, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Extracellular sucrase (EC 3.2.1.26) (Beta-fructofuranosidase)
(Invertase) (Saccharase) (Protein B46).
SACC OR INVB OR SUCE3.
                                                                                                                                                                                                                                                                                                                                                             Song K.B., Lee S.K., Joo H.K., Rhee S.-K.;
Nuclectide and derived amino acid sequences of an extracel
sucrase gene (InvB) of Zymomonas mobilis ZMI (ATCC10988).";
Blochim. Biophys. Acta 1219:163-166(1994).
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                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-ATCC 10988 / ZM1;
MEDLINE-94368848; PubMed-8086457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-NRRL B806;
MEDLINE-95297907; PubMed-7778976;
                                                                  InterPro; IPR003469; Glyco_hydro_68.
Pfam; PF02435; Glyco_hydro_68; 1.
                                                    GNYATWAPSFLVOINPDDTTTVLARATNOG
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-IFO 13756;
MEDLINE-95218269; PubMed-7766026;
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STRAIN-ATCC 31821 / ZM4 / CP4;
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L33403; AAC36942.1;
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CONFLICT 85 85
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               NCBI_TaxID=542;
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STRAIN=IFO 13756;
MEDLINE=95218269; PubMed=7766026;
Kyono K., Yanase H., Tonomura K., Kawasaki H., Sakai T.;
Kyono K., Tonomura K., Kawasaki H., Sakai T.;
Kyono K., Sakai T.;
Kyono K., Sakai T.;
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Kyono K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 IFGTKETNVFQEWSGSAIV--NDDGTIQLFFTSNDTSDYKLNDQRLATATL---NLNVDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 EGVWFKGFDQSTDLFQADGLFYQNY-----AENNLWNFRDPHVFINPEDGETYALFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413 ANTGTEDYQSDDQIYNWANYGGDDAFNIKSSFKLLNNKKDRELAGLANGALGILKLTNNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  473 SKPKVE-EVYSPLVSTLMACDEVXXK----LGDKYYLFSVTRVSRGSDRELTAKDNTIVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          528 DNVAMIGYVSDS-LMGKYRPLNNSGVVLTASVPANWRTATYSYYAVPVAGHPDQVLITSY
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060114; 060116; Q06487;
15-DEC-1998 (Rel. 37, Crasted)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Levansucrase (EC 2.4.1.10) (Beta-D-fructofuranosyl transferase)
6 Sucrose 6-fructosyl transferase).
Zymomonas mobilis.
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                                                                                                                                                                                                                                                                                                DB 1; Length 413;
                                                                                                                                                                                                                                                                                                                                                                                         71; Mismatches 150; Indels
    S -> L (IN REF. 2).
T -> S (IN REF. 2).
PVWP -> LGMA (IN REF. 3).
BACC12D167332E47 CRC64;
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Gunasekaran P., Mukundan G., Kannan R., Velmurugan S.,
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                                                                                                                                                                                                                                                                                      Score 309; DB 1
Pred. No. 9e-10;
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STRAIN-ATCC 10988 / ZM1;
MEDLINE-93305726; Pubmed-8318541;
                                                                                                                                                MW.
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les 105; Conservative
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413 AA;
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SACB_RAHAQ
O54435;
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                                                                   SACB_RAHAO
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                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 SVNDTP----SESVPAQCKGYIYADDKSVWFDGFDKVTDLFQADGLYYADY-----A 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 ENDDYCLRDPHV-VQLENGDRYLVFEANTGTEDYQSDDQIYNWANYGGDDAFNIKSSFKL 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSQPYQAYSHYVM-----TNGLVTSFIDT--IPSSDPNVYRYGGTLAPTIKLELVGHRS 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 DAQTGKMAHLD-----GIPN 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 DDPTATMPTIDYDFPVMTDKYWVWDTWPLRD-INGQVVSFQGWSVIFALVADRTKYGWHN 82
                                                                                 Ahn J.Y., Kang H.S.; "Sequence analysis of 44B6 fosmid clone of Zymomonas mobilis ZM4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTVLARATN----QGDWVWDDSSRNDNMLGVLKEGAANSAALPGEWGKPVDWSLINR 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 LTYLFTISHHSTYAD-GLSGPD-----GVYGFVSENGIFGPYEPLNGSGLVL--GNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 SPTGDNHIYLLYNKYGDNDFSHWRNAGSIFGTKETNVFQEWSGSAIV--NDDGTIQLFFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNDG-ARIGYFYSRGGSN----WIFGGHLLKDGANPRSWEWSGCTIMAPGTANSVEVFFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 S-NDTSDYKLNDQRLATATLNLNVDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         447 LNNKKDRELAGLANGALGILKLINNQSKPKVE-EVYSPLVSTLMACDE-----VXXKLGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          501 KYYLFSVTRVSRGSDRELTAKDNTIVGDNVAMIGYVSDS-LMGKYKPLNNSGVVLTASVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANWRTATYSYAVPVAGHPDQVLITSYMSNKDFASGEGNY ----ATWAPSFLVQINPDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 423;
                                                                                                                                                           ALSO ACT AS FRUCTOSTL ACCEPTORS).
-1- SUBCELLULAR LOCATION: Secreted.
-1- PTM: DOES NOT SEEM TO BE N-TERMINALLY PROCESSED.
-1- SIMILARITY: BELONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F. 2).
(IN REF. 1 AND 4).
                                                                                                               Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: SUCROSE + (2,6-BETA-D-FRUCTOSYL)(N)
GLUCOSE + (2,6-BETA-D-FRUCTOSYL)(N+1) (OTHER SUGARS CAN
Ait-Abdelkader N., Alvarez E., Barattl J.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19A4691DA3EB9FE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 251.5; DB 1
; Pred. No. 1.1e-06;
76; Mismatches 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V -> I (IN REF.
NPED -> TPKI (IN
E -> Q (IN REF.
T -> A (IN REF.
C -> Y (IN REF.
I -> V (IN REF.
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2ro; IPR003469; Glyco_hydro_68.
PF02435; Glyco_hydro_68; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF081588; AAA27695.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46762 MW;
                                                                 31821 / ZM4 / CP4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.1%;
                                                                                                                                                                                                                                                                                                                                                                                                         D17524; BAA04475.1;
L33402; AAA27702.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.1
Best Local Similarity 24.3
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 AA;
                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase;
CONFLICT
                                                                 STRAIN-ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NHIYL------LYNKYGDNDFSHWRN-----AGSIFGTKETNVFQEWSGSAI 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -VNDDGTIQLFFTSNDTSDYKLNDQRLATATLNLNVDDNGVSIKSVDNYQVLFEGDGFHY 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSEYLDAEGNYDITSDWNNRHGRARICYWYSRTGKDWIFGGRVMAEGVSPTSREWAGTPI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QTYEQFANGKDRENDDYCLRDPH-VVQLENGDRYLVFEANTGTEDYQSDDQIYNWANYGG 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDAFNIKSSFKLLNNKKDRELAGLANGALGIL---KLTNNQSKPKVEEVYSPLVSTLMAC 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHVIGKQEMGTLPPGHRDVGNARYQAGCIGMAVAKDLSGDE-----WEILPPLVTAVGVN 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVXXK----LGDKYYLFSVTRVSRGSDRELTAKDNTIVGDNVAMIGYVSDSLMGKYKPL 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90;
                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Levansucrase (EC 2.41.10) (Beta-D-fructofuranosyl transferase)
(Sucrose 6-fructosyl transferase).
----STTNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression, and levan formation.";
Ann. N.Y. Acad. Sci. 864:506-511(1998).
-!- CATALYIT ACTIVITY: SUCROSE + (2,6-BETA-D-FRUCTOSYL)(N)
GLUCOSE + (2,6-BETA-D-FRUCTOSYL)(N+1) (OTHER SUGARS CAN
ALSO ACT AS FRUCTOSYL ACCEPTORS).
-!- SIMILARITY: BELONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Song K.B., Seo J.W., Kim M.G., Rhee S.K.; "Levansucrase of Rahnella aquatilis ATCC33071. Gene cloning,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 415;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro: IPR003469; Glyco_hydro_68.
Pfam: PP02435; Glyco_hydro_68; 1.
Transferase; Glycosyltransferase;
SEQUENCE 415 AA; 45939 WW; E028828813D13A74 CRC64;
---SAAAL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred. No. 2.3e-06; 72; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.9%; Score 245; DB 1; 33.8%; Pred. No. 2.3e-06;
                                                                                                                                                                   Ź
                                                                                                                                                                   415
                                                                                                                                                                   PRT;
389 FVTEVKGYGYIPPQIEWLAEDESSN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ATCC 33071;
MEDLINE-99127094; PubMed-9928133;
                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequ
30-MAY-2000 (Rel. 39, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U91484; AAC36458.1; -.
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Matches 100; Conservative
                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            Rahnella aquatilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                      384
 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hettwer U., Jaeckle E.R., Boch J., Meyer M., Rudolph K., Ullrich M.S.
"Cloning, nucleotide sequence, and expression in Escherichia coli of levansucrase genes from the plant pathogens Pseudomonas syringae pv. plant pathogens Pseudomonas syringae pv. Appl. Environ. Microbiol. 64:3180-3187(1998).
-!- CATALYTIY: SUCROSE + (2,6-BETA-D-FRUCTOSYL)(N) - GLUCOSE + (2,6-BETA-D-FRUCTOSYL)(N+1) (OTHER SUGARS CAN ALSO ACT AS FRUCTOSYL ACCEPTORS).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---YNKYGDNDFSHWRNAGSIFGTKETNVFQEWSGS-AIVNDDGTIQLFFTSNDTSDYKL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H-VVQLENGDRYLVFEANTGTEDYQSDDQIYNWANYGGDDAFNIKSSFKLLNNKKDRELA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPFIDPNDGKLYMVFEGNV------AGERGTHTVGAAELGPVPPGHEET 247
548 NNSGVVLTASVPANWRTATYSYYAVPVAGHPDQVLITSYMSNKDFASGEGNY---ATWAP
                       --AAIAKVRGRIVTSDKGVELKDFTEVKTLFEADGKYYQT------EAQNSTWNFRDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYWYSRIGKD----WIFGGRVMAEGVSPTTREWAGTPVLLNDKGDIDLYYTCVTPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NDQRLATATLNLNVDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDRENDDYCLRDP
                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Levansucrase (EC 2.4.1.10) (Beta-D-fructofuranosyl transferase)
(Sucrose 6-fructosyl transferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89;
                                                                                                                                                                                                                                                                                                                                                 Pseudomonas syringae (pv. glycinea).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 VWDSWPVQDPVTGYVSNYMGYQLVIAMMG--IPNSP--TGDNHIYLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.8%; Score 242.5; DB 1; Length 23.6%; Pred. No. 3.2e-06; ive 68; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            839B686AC80610CF CRC64;
                                                                                                                                                                                                      415 AA
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Pfam; PF02435; Glyco_hydro_68; I.
Transferase; Glycosyltransferase
SEQUENCE 415 AA; 45844 WW; 839B6
                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98394981; PubMed-9726857;
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                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=318;
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                                                                                                                                                                                                      PSESG
                                                                       605 S 605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----HKFTYADGVTGPDGV--YGFVGEHLFGPYRPMNASGLVL-GNPPAQ-PFQTYSHCV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDNDFSHWRN-----AGSIFGTKETNVFQEWSGSAI-VNDDGTIQLFFTSNDTSDYK 336
GLANGALGILKLINNQSKPKVE-EVYSPLVSTLMACDEVXXK----LGDKYYLFSVTRVS 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 GRARMSYWYSRTGKDWIFGGRVMAEGVSPTTREWAGTPILLNDKGDIDLYYTCVTPG---
                                                                                                             RGSDRELTAKDNTIVGDNVAMIGYVSDSLMGKYKPLNNSGVVLTASVPANWRTATYSYYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNDQRLATATLNLNVDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDRENDDYCLRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Levansucrase (EC 2.4.1.10) (Beta-D-fructofuranosyl transferase)
(Sucrose 6-fructosyl transferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rseudomonas syringae (pv. phaseolicola).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               431;
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                                                                                                                                                                                                                                572 VPVAGHPDQVLITSYM----SNKDFASGEGNYATWAPSFLVQINPD 613
                                                                                                                                                                                                                                                                    EMBL; AF052289; AAC36063.1; -.
InterPro; IPR003469; Glyco_hydro_68.
Pfam; PF02435; Glyco_hydro_68; 1.
Transferase; Glycosyltransferase.
SEOUENCE 431 AA; 47603 MW; 795FEA246D40C40F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%; Score 240.5; DB 1; 23.3%; Pred. No. 4.2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        431
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-NCPPB 1321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SACB_PSESH
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--ATIAKVRGKIVTSDQSVSLEGFQQVTSLFSADGTIYQTEEQ-----NAFWNFRDP 204
                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=33996;
                                                                                                                                                                                                                                                                              SACB_ACEDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 INDIMPLRD-FDGEIISVNGWCIIFTLTADRNTDNPQFQDENGNYDITRDWEDRHGRARI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NDQRLATATLNLNVDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDRENDDYCLRDP 397
                                                                   SRGSDRELTAKDNTIVGDNVAMIGYVSDSLMGKYKPLNNSGVVLTASVPANWRTATYSYY 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Characterization and infuence on virulence of the levansucrase gene from the firstblight pathogen Erwind amylovora.";
Physiol. Wol. Plant Patholo. 42:387404(1993).
-I-CATALYTIC ACTIVITY: SUCROSE + (2,6-BETA-D-FRUCTOSYL)(N) = GLUCOSE + (2,6-BETA-D-FRUCTOSYL)(N) = ALSO ACT AS FRUCTOSYL ACCEPTORS).
-I-SUBCELLULAR LOCATION: Secreted.
-I-SUBCELLULAR ELOCATION: Secreted.
 PH-VVQLENGDRYLVFEANTGTEDYQSDDQIYNWANYGGDDAFNIKSSFKLLNNKKDREL 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --GDNHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 YLLYNKYGDNDFSHWRNAGSIFGTKETNVFQEWSGSAI-VNDDGTIQLFFTSNDTSDYKL
                           ----AGERGSHTVGAAELGPVPPGHED
                                                    456 AGLANGALGILKLINNQSKPKVE-EVYSPLVSTLMACDEVXXK----LGDKYYLFSVTRV
                                                                                                                                  323 FTYAE-GLIGPD-----GVYGFVGEHLFGPYRPMNASGLVL--GNPPEQPFQTYSHC
                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Levansucrase (EC 2.4.1.10) (Beta-D-fructofuranosyl transferase)
(Sucrose 6-fructosyl transferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.7%; Score 236.5; DB 1; Length 415;
                                                                                                                                                                             :| :||:|: : | 372 VMP-----NGLVTSFIDSVPTEGEDYRIG----GTEAPTVRILLKGD 409
                                                                                                                                                            571 AVPVAGHPDQVLITSYMSN-----KDFASGEGNYATWAPSFLVQINPD 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR003469; Glyco_hydro_68.
Pfam: PF02435; Glyco_hydro_68.
Transferase; Glycosyltransferase
SEQUENCE 415 AA; 46408 MW; 4FF564F6E0607FEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .6e-06;
es 152;
                                                                                                                                                                                                                                                       415 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 VWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred. No. 6.6e
67; Mismatches
                                                                                                                                                                                                                                                                                (Rel. 37, Created)
(Rel. 37, Last seq
                             PSPFIDPNDGKLYMVFEGNV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X75079; CAA52972.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 23.49
Matches 96; Conservative
                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              Erwinia amylovora
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=552;
                                                                                                                                                                                                                                                       ERWAM
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-EA7,
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                                                                                                                                                                                                                                                                                                                                                                                       Erwinia
                                                                                                                                                                                                                                                                     046654;
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                                                                                                                                                                                                                                                                                                                                      305 -----HKYYFADNLTGPDGV--YGFVSDKLTGPYTPMNSSGLVL--GNPSSQPFQTYS 353
                                                                                                                                                                                                                                                                                              RVSRGSDRELTAKDNTIVGDNVAMIGYVSDSLMGKYKPLNNSGVVLTASVPANWRTATYS 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microbiology 142:1077-1085(1996).
-I- FUNCTION: RELEASES FRUCTOOLIGOSACCHARIDES AND LEVAN, A HIGH-MOLECULAR-MASS FRUCTOSYL POLYMER, FROM SUCROSE. IT ACTS MORE AS
                                                                                                                                                                                            Arrieta J., Hernandez L., Coego A., Suarez V., Balmori E., Memendez C., Petitt-Glatron M.-F., Chambert R., Salmar-Housein G.; Molecular characterization of the levansucrase gene from the endophytic sugarcane bacterium Acetobacter diazotrophicus SRT4.";
398 H-VVQLENGDRYLVFEANT----GTEDYQSDDQIYNWANYGGDDAFNIKSSFKLLNNKKD
                                                                      SPFIDRNDGKLYMLFEGNVAGPRGSHEITQ-----AEMG-----NVPPGYEDVGGAKY
                                                                                                                                             453 RELAGLANGALGILKLINNQSKPKVEEVYSPLVSTLMACDEVXXK----LGDKYYLFSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.7%; Score 197; DB 1; Length 584;
23.8%; Pred. No. 0.0013;
tve 78; Mismatches 175; Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acetobacter diazotrophicus (Gluconacetobacter diazotrophicus).
Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
Gluconacetobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Levansucrase precursor (EC 2.4.1.10) (Beta-D-fructofuranosyl transferase) (Sucrose 6-fructosyl transferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALSO ACT AS FRUCTOSYL ACCEPTORS).
SUBCELLULAR LOCATION: Secreted.
PTM: THE N-TERMINAL IS BLOCKED.
SIMILARITY: BELONGS TO FAMILY 68 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUCROSE HYDROLASE THAN AS A FRUCTAN POLYMERASE.
CATALYTIC ACTIVITY: SUCROSE + (2,6-BETA-D-FRUCTOSYL)(N)
GLUCOSE + (2,6-BETA-D-FRUCTOSYL)(N+1) (OTHER SUGARS CAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 HYVMP-----NGLVTSFIDSVPWKGKDYRIG----GTEAPTVKILLKGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                    569 YYAVPVAGHPDQVLITSYMSN-----KDFASGEGNYATWAPSFLVQINPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CBFBF4139AD0B8CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       584 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 52-61.
STRAIN-SRT4 / CBS 550.94;
MEDLINE-96253999; PubMed-8704949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L41732; AAB36606.1; -. InterPro; IPR003469; Glyco_hydro_68. Pfan; PPF0445; Glyco_hydro_68; 1. Transferase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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Best Local Similarity 23.8%;
Matches 117; Conservative 7
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9

SIMILARITY: CONTAINS 1 SAM DOMAIN

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tyrosine phosphate.

DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT DEVELOPMENT WITH A PEAK
                                                                                                                                                                                                                                                                                                                                                                                                                    EGDGFHYQTYEQFANGKDRENDDYCLRDPHVVQ--LENGDRYLVFEANT----GTEDYQS 422
                                                                                                                                                                                                                                                              423 DDQIYNWANYGGDDAFNIKSSFKLLNNKKDRELA--GLANGALGILKLTNNQSKPKVEEV 480
                                                                                                                                                                                                                                                                                           342 AD-----IGFRPNDP-NAETLQEVLDSGAYYOKANIGLA-----IATDSTLSKWK---F 386
NMPATYTVDAQTGKMAHLD--VWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPTG--D 275
                                                                                                                              VND--DGTIQLFFT----SNDTSDYKLN-DQRLATATL-NLNVDDNGVSIKSVDNYQVLF 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Non-receptor tyrosine kinase spore lysis A (EC 2.7.1.112) (Tyrosine-
                                                                                                                                                                                                                 290 QPDGVLYQ-----NG--AQNEFENFRDPFTFEDPKHPGVNYMVFEGNTAGQRGVANCTE
                                                                                                                                                  : | : | : | : | : | 330 IMQIHGNTVSVFYTDVAFNRDANANNITPPQAIITQTLGRIHADFNHVWFTGFTAHTPLL
                                                                                                                                                                                                                                                                                                                               481 YSPLVSTLMACDEVXXKL----GDKYYLFSV---TRVSRGSDRELTAKDNTIVGDNVAMI
                                                                                                                                                                                                                                                                                                                                                              .-----GPD-GVY
                                                                                                                                                                                                                                                                                                                                                                                               ----TYSYYAVPVAG
                                                               ----YGDNDFSHWRNAGSIFGTKETNVFQEWSGSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HPDQVLITSYMSNKDFASGEGNYATWAPSFLVQINPDDTTTVLARATNQGDWVWDD--SS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DURING THE MOUND STAGE OF MORPHOGENESIS.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES BUT ALSO TO
SERINE/THREONINE PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuckolls G.H., Osherov N., Loomis W.F., Spudich J.A.; "The Dictyostellum dual-specificity kinase splA is essential spore differentiation."; Development 122:3295-3305(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-90287147; PubMed-1972546;
MEDLINE-90287147; PubMed-1972546;
MEDLINE-90287147; PubMed-1972546;
MEDLINE-902871417; PubMed-1972546;

"Developmentally regulated protein-tyrosine kinase genes Dictyostellum discoldeum.";

Dictyostellum discoldeum.";

-1. FUNCTION: ESSENTIAL FOR SPORE DIFFERENTIATION.

-1. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dictyostellum discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID-44689;
                                                                                                                                                                                                                                                                                                                                                                387 LSPLISANCVNDQTERPQVYLHNGKYYIFTISHRTTFAAGVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1584 AA
                                                                                                                                                                                                                                                                                                                                                                                                 GYVSDSLMGKYKPLNNSGVVLTASVPANWRTA----
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MEDLINE-97053827; PubMed=8898241;
                                                              276 NHIY----LLYNK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein kinase 1).
PYKA OR SPLA OR DPYK1.
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RADVNIAGFIQD 554
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P18160;
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                           between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STSIL------VPNGNNNNSNNNNNNNNNNIIG-NGKITTTTTTTSPSSINNN 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QESSATNNTENAVVNESKNTNNTENAVVNENKNTNNTENAVVNENKNTNNTENDNSQLKL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAEKGAKLTFKDLEGIGN--AIVKQ-DPQYAIPYSNAKEIKNMPATYTVDAQTGKMAHLD 238
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                                                                                                                                                                                                                                                                                                                                                                                  1.
kinase; ATP-binding; Phosphorylation.
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9.3%; Pred. No. 0.011;
ve 103; Mismatches 283; Indels 303;
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> L (IN REF. 2).
5D1589458D8E01E3 C
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ATP (BY SIMILARITY)
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POLY -BHE.
POLY - SER.
POLY - SER.
POLY - GLN.
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POLY - PRO.
POLY - PRO.
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D -> R (IN RE
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POLY-ASN.
POLY-ASN.
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POLY-ASN.
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                                                                                                                                                                                                                                       InterPro; IPR004040; STY_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam: PF00069; pkinase; 1.
                                                                                                                                                                     Dictybb, DD03010; pyka.
InterPro; IPR000719; Euk_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
4.6%; Sco
Best Local Similarity 19.3%; Pro
Matches 165; Conservative 103;
                                                                                                                                                                                                                                                                                                                                                                                            Tyrosine-protein
                                                                                                                       EMBL; U32174; AAB41125.1; -.
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                                                                                                                        EMBL; M33785; AAA33202.1;
PIR; A35670; A35670.
HSSP; P11362.
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Pfam; PF00536; SAM; 1.
Pfam; PF00622; SPRY; 3.
SMART; SM00454; SAM; 1.
SMART; SM00449; SPRY; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          702 GNGDK---PAGKATPDNTNI------DPSAQPSGQNTNIDP----SAQXSGQ 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   901 QGSG-FKNWAP-----NDVAIWLESFNYGO--YRKNFRDNNISGRHLEGITH-AML 947
                                                                                                                                                                                                                                                                                                                                                                                         454
                                                                                                                                                                                                                                                                                                                                                                                                                                              KDDITLTIIKKKTSVA-------MADRPFSSNSSSTICYFEVYLEGHDKKGSI 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   654 PGEWGKPVDWSLINRSPGLGLKPHQPVQPKIDQ-------PDQQPSGQNTKNVTP 701
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                                                                                                                                                                                                                                                                                                               864 VGGLCVATFPGGHFRFNIEDLPGISPSVWTEAL------GPDR------
                                                                                                                                                                                                                                                                           GVSIKS-------VDNYQVLFEGDGFHYQTYEQFANGKDRENDDYCLRDPHVVQL
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                                               239 VWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPTGDNHIYLLYNKYGDNDFSHWRNAGS
                                                                                                        ----TTAGS
                                                                                                                                                             ---IFGTKETNVFQEWSGSAIVNDDGTIQLFFTSNDTSDYKLNDQRLATATLNLNVDDN-
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01-JAN-1990 (Rel. 13, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
AAC-rich mRNA clone AAC11 protein (Fragment).
Dictyostellum discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
562 NSSSGS-----IGNNSSIIKQRSPPHSI-----NGP---
                                                                                                     -----LMLPPSSTNNNNIYSSYNS-
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P14196;
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AAC2_DACA
AC P14196
DT 01-JAN
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                                                                                                                                                                                                                                                                                                                                                                                                     7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTENAVVNESKNTNNTENAVVNENKNTNNTENAVVNENKNTNNTENDNSQLKLTNNEQPS 138
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Igarashi T., Yamamoto A., Goto N.;
"Sequence analysis of the Streptococcus mutans Ingbritt dexA gene encoding extracellular dextranase.";
Microbiol. Immunol. 39:853-860(1995).
                                                                                                                                                                                                                                                                                                                                                                                                       50;
                                                                                                                                                                                                                                                                                                                                                                     Query Match 4.6%; Score 190; DB 1; Length 448; Best Local Similarity 25.3%; Pred. No. 0.0022; Matches 56; Conservative 30; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colby S.M., Whiting G.C., Tao L., Russell R.R.B.; "Insertional inactivation of the Streptococcus mutans dexa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Dextranase precursor (EC 3.2.1.11) (Alpha-1,6-glucan-6-
                                                                                                                                                                                                                                                                                                            ASN-RICH.
D8FD80D910D99817 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 N-----AIVKQDPQYAIPYSNAKEIKNMP-ATYTVDAQ 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407 NLGNLGRVSGLHSSDP-----NNPNAQKSFPDSTNTMDFQ 441
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ASN-RICH.
                                                                                                                                                                                                    Pfam; PF02178; AT_hook; 4.
ProDom; PD005593; Highmoblty_IY; 1.
                                                                                                                                                                                       Highmoblty_IY
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MEDLINE-96081507; PubMed-8535521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96245544; PubMed-8657012;
                                                                                                                                                                                                                                                                                                                             48636 MW;
                                                                                                                                                                       InterPro; IPR000637; AT_hook InterPro; IPR000116; Highmob
                                                                                                                            EMBL; X16522; CAA34529.1; -.
                                                                                                                                                                                                                                  SMART; SM00384; AT_hook; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                              S05355.
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115
268
448 AA;
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                                                                                                                                                          DictyDb; DD05006;
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NCBI_TaxID=1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-INGBRITT;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55;
                 catabolism.";
Microbiology 141:2929-2936(1995).
-!- FUNCTION: MAY PLAY A ROLE IN SUCROSE-INDEPENDENT ADHERENCE TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 TNNTENAVVNESKNTNN-----TENAV-----VNENKNTNNTENAVVNENKNTN--N 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 AHADQVESNNYNGVAEVNTERQANGQIGVDGKIISANSNT-----TSGSTNQESS---A 76
                                                                                                                                                            SUBCELLULAR LOCATION: Type I membrane protein. Cell wall. STMILARITY: TO OTHER STRREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR. SIMILARITY: BELONGS TO FAMILY 66 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 AAAVQTES-----ASIDSNEQEQS------VSANTNTQPQAKKLSNNSHQEPMQMVS
                                                                                         CATALYTIC ACTIVITY: Endohydrolysis of 1,6-alpha-D-glucosidic linkages in dextran. SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.5%; Score 185; DB 1; Length 850; Best Local Similarity 21.0%; Pred. No. 0.0094; Matches 201; Conservative 108; Mismatches 290; Indels 358;
(dextranase) gene results in altered adherence and dextran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D653CAA39C93D2AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001899; Gram_pos_anchor.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
Hydrolase; Glycosidase; Signal; Transmembrane.
                                                                             PELLICLE-COATED TOOTH SURFACE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             850 AA; 94538 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D49430; BAA08409.1; -.
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TRANSMEM
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122 TENDNSQLKLTNNEQPSAATQANLKKLNPQAAKAVQNAK--IDAGSLTDDQINELNKINF 179
                              192 SDSQNNILEQGNRAIAVEDDWRTFPRYAAIGGSQKDNNSVLTKNLPDY---YRELEQMKN 248
                                                                                                                                                                                                                                              284
                                                                                                                                                                                                                                                                                                                                                     285 YGDNDFS-HWRN--AGSIFGTKETNVFQEWSGSAIVNDDGTIQLFFTSNDTSD----YKL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 YYYNPLSKSWONYISNAMAQAMKTGGFDGWQGDTI--GDNRV-LSHNQKDSRDIAHSFML 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ND------QRLATATLNLNVDDNGVSIKSVDN-----YQVL--FEGDGFHYQTYE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             380 QFANGKDRENDDYCLRDPHVVQLENGDRYLV-----FEAN------TGTEDY 420
                                                                                                         SKS----AEKGAKL------TFKDLEGIG-----NAIVKQDPQYAIPYSNAKEIKN
                                                                                                                                                                                                                MPAT----YTV------OTGKMAHLDV
                                                                                                                                                                                                                                                                                                                      240 WDSWPVQD-----PVTGYVSNYM--GYQLVIAMMGIPNSPTGDNHIYLLYN-----K
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QQ	469	469 SYGDLKARVDQVRQATGKSLIVGAYMEEPKFDDNRIPLNGAARDVLASATY 519	519
ογ	421	QSDDQIYNWANYGGDDAFNIKSSFKLLNNKKDRELAGLANGALGILKLTNNQSKPK	476
QQ	520		556
ογ	477		530
qq	557	557 -ETAYYPTQSLKVSKELNRKNYHYQQFITAYEN-LLRDKVENDSAE	009
δλ	531	531AMIGYVSDSLMGKYKPLNNSGVVLTASVPANWRTATYSYYAVPVAGHPDQVL	582
QO	601	~	642
οy	583	-ITSYMSNKDFASGEGNYATWAPSFLVQINPDDTTTVLARA	622
qq	643	643 GITSDWKNEDGYENNKTPDEQTNLLVTYPLTGVSMAEADRIAKQVYL 689	689
δy	623	INQGDWVWDDSSRNDNMLGVLKEGAANSAALPGEWGKPVDWSLINRSPG	671
QQ	069	TSPDDWLQSSMISLTTQVKTNENGDPVLYIQVPRLTLWDMIYINET	735
οy	672	PSGONTK	731
qq	736		780
οy	732	732 DPSAQX-SGONTKNVTPGNEKQGKNTDAKQLPQTGNKSGLAGLYAGSLLALFGLAAI 787	
QQ	781	: : : : : : : : : : : : : : : : : : :	_

Search completed: September 26, 2002, 18:26:47 Job time: 186 sec

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September 26, 2002, 18:25:06; Search time 40.2 Seconds (without alignments) 1893.103 Million cell updates/sec
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                                                                                                                                                                                                                                              1 MYKVGKNWAVATLVSASILM......LYAGSLLALFGLAAIEKRHA 792
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                   283138 seqs, 96089334 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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4149
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Maximum DB seq length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*
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Perfect score:
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	Description	levansucrase (EC	levansucrase (EC 2	levansucrase (EC 2	levansucrase [impo	levansucrase [impo	н	extracellular sucr	levansucrase (EC 2	levansucrase - Zym	levansucrase - Erw	zeq	hypothetical prote	fibrinogen-binding	ŝ			cal	₽	hypothetical prote	protein-tyrosine k	hypothetical prote	membrane nuclease,	idrug re	e Du	hypothetical prote	hypothetical prote	probable autotrans	rinogen-bindi	HPI layer surface
SUPERALES	ID	B28551	JQ0802	A25040	F97118	Π	$^{\circ}$	S47527	JC2519	S33771	S39195	B97033	AH2515	T28680	\$22737	B86748	AG2560	E89824	AE1525	T18491	T18276	S05355	E90598	T18267	T30290	C89921	T18444	AD0123	83	83
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æ		40.6	18.1		16.5		7.4	7.0		5.8	5.7	•	6.4	4.8	4.8	4.7	4.7	4.7	4.7	4.6	4.6	4.6	4.6	4.5	4.4	4.4	4.4	4.4	4.4	4.4
	Sco	1684.5	751.5	746.5	685.5	315	308	292	249.5	242.5	236.5	203.5	203.5	199.5	198.5	195.5	194	193.5	193	191.5	9	190	189	185	184	183	8	182.5	182	182

glucosyltransferas hypothetical prote hypothetical prote internalin protein cell surface glyco collagen adhesin - hypothetical prote fibrinogen-binding glucosyltransferas hypothetical prote cell surface glyco hypothetical prote dextranase - Strep dipoprotein [impor	Clumping ractor b hypothetical prote
T30552 B89921 B8417 AD1095 B84417 B84417 B842404 T28679 T28679 T28679 T28679 T28679 T28679 T28679 T28679 T28679 T28679 T28679 T28679 T296537	F90070 AH2282
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182 182 182 181 181 179 5 179 179 178 178 178 178	177.5
0 H G W 4 4 4 4 4 4 4 6 0 H G W 4 7 0 0 0 0 1 G K 8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	<b>4</b> 4 5

## ALIGNMENTS

ain GS-5) 15-Oct-1999 transferase gene and :g153636	197; 109; Gaps 21;	/DGKIIS 60	/ 113   118 	NVQNAKI 161 	AKEIKNM 221          AKAIKNM 228	ONHIYLL 281          ONHIYLL 286	KKLNDQR 341  :   KNSNNQR 346	DDYCLRD 396  : :   DNIAMRD 402	KKDRELA 456 :
RESULT 1 B28551 B28651 B28651 B28651 N;Alternate names: sucrose 6-fructosyl transferase C;Species: Streptococcus mutans C;Species: Streptococcus mutans C;Species: Streptococcus mutans C;Accession: B28551 B;Shiroza, T.; Kuramitsu, H.K. J. Bacteriol. 170, 810-816, 1988 A;Title: Sequence analysis of the Streptococcus mutans fructosyltransferase A;Title: Sequence analysis of the Streptococcus mutans fructosyltransferase A;Reference number: A91892; MUID:88115184 A;Molecule type: DNA A;Residues: 1-797 <shi>A;Residues: 1-797 <shi>A;CSHI C;Keywords: glycosyltransferase; hexosyltransferase</shi></shi>	Query Match 40.6%; Score 1684.5; DB 2; Length 797; Best Local Similarity 44.3%; Pred. NO. 8.2e-86; Matches 370; Conservative 126; Mismatches 230; Indels 109;	1 MYKVGKNWAVATLVSASILMGGVVTAHADQVESNNYNGVAEVNTERQANGOIGVDGKIIS 	61 ANSNITSGSTNQESSATNNIENAVVNESKNINNTENAVVNENKNIN-NTENAVV	114NENKNTNNTENDNSQLKLTNNEQPSAAT-QANLKKLNPQAAKAVQNAKI ::	162 DAGSLIDDQINELNKINFSKSAEKGAKLIFKDLEGIGNAIVKQDPQYAIPYSNAKEIKNM :	222 PATYTVDAQTGKMAHLDVWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPTGDNHIYLL 	282 YNKYGDNDFSHWRNAGSIFGTKETNVFQEWSGSAIVNDDGTIQLFFTSNDTSDYKLNDQR 	342 LATATLNLNVDDNGVSIKSVDNYQVLF-EG-DGFHYQTYEOFANGKDRENDDYCLRD	397 PHVVQLENGDRYLVFEANTGTEDYQSDDQIYNWANYGGDDAFNIKSSFKLLNNKKDRELA 456
RESULT 184851 187851 187851 177851 177951 177951 1771 1771 1771 1771 177	Query Best Match	Qy .	Qy Db	Qy 1 Db 1	Qy 1 Db 1	Oy 2 Db 2	Qy 2 Db 2	Oy 3 Db 3	oy 3

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A;Residues: 1-473 <KUN>
A;Cross-references: GB:299121; GB:AL009126; NID:g2635827; PIDN:CAB15450.1; PID:g26359
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                               607 LVQINPDDTTTVLARATNQG 626
                                                                                                                                                                                                                                                                                                                                                                                                448 LMNIKGNKTSVVKNSILEQG 467
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N;Alternate names: 2,6-beta-D-fructan-6-beta-D-fructosyltransferase; sucrose
C;Specia: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 15-oct-1999
C;Accession: JQ0802; S11739
R;Tang, L.B.: Lenstra, R.; Borchert, T.V.; Nagarajan, V.
Gene 96, 89-93, 1990
A;Tile: Isolation and characterization of levansucrase-encoding gene from Bacillus amyl
A;Reference number: JQ0802; MUID:91092506
A;Accession: JQ0802
A;Molecule type: DNA
A;Restence unmber: JQ0802; MUID:91093333; PIDN:CAA37179.1; PID:g39334
A;Rectoss: EMBL:X52988; NID:g39333; PIDN:CAA37179.1; PID:g39334
A;Cossion: Sacues: 1-472
A;Coss-references: EMBL:X52988; NID:g39333; PIDN:CAA37179.1; PID:g39334
A;Coss-references: EMBL:X52988; NID:g39334
A;Coss-references: EMBL:X52988; NID:g39333; PIDN:CAA37179.1; PID:g39334
A;Coss: references: EMBL:X52988; NID:gadacted <SIC-File: File: F
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103 PHVIEDENGDRYLVFEASTGTENYQGEDQIYNFTNYGGSSAXNVKSLFRFLDDQDMYNRA 462
                                                                                                                                                                                      692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     693 GQNT------KNVTPGNGDKPAGKATPDNTNIDPSAQPSGQ 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          688 VPSTPIHTDDIISFEVSFDGHLVIKPVKVNNDSAGRIDQSRNSGGSLNVAFNVSA---GG 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 NLKKLNPQAAKAVQNAKIDAGSLTDDQINELNKINFSKSAEKGAKLTFKDLEGIGNAIVK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QDPQYAIPYSNAKEIKNMPATYTVDAQTGKMAHLDVWDSWPVQDPVTGYVSNYMGYQLVI 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FHYQTYEQFAN-GKDRENDDYCLRDPHVVQLENGDRYLVFEANTGTED-YQSDDQIYNWA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLANGALGILKLTNNQSKPKVEEVYSPLVSTLMACDEV----XXKLGDKYYLFSVTRVSR
                                                                                                                                                                                                                                                              PVAGHPDQVLITSYMSNKDFASGEGNYATWAPSFLVQINPDDTTTVLARATNQGDWVWDD
                                                                                                                                                                                                                                                                                                                                                                  633 SSRNDNMLGVLKEGAANSAALPGEWGKPVDWSLINRSPGLGLKPHQPVQPKIDQPDQQPS
                                                                                  GSDRELTAKDNTIVGDNVAMIGYVSDSLMGKYKPLNNSGVVLTASVPANWRTATYSYYAV
                                                                                                                                                                                                                                                                                                                                                                                                   AMMGIPNSPTGDNHIYLLYNKYGDNDFSHWRNAGSIFGTKETNVF------QEWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            728 NTNIDPSAQXSGQNTKNVTPGNEKQGKNTDAKQLPQTGNKSGLAGLYAGSLLALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 472;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.1%; Score 751.5; DB 2;
38.0%; Pred. No. 2.2e-34;
tive 88; Mismatches 171;
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Best Local Similarity 38.0%
Matches 190; Conservative
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Nationary No. 2011. No. 9 actor precursor - Bacillus subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss leavant subtliss subtliss subtliss leavant subtliss subtliss leavant subtliss subtliss subtliss leavant subtliss subtliss leavant subtliss subtliss leavant subtliss subtliss leavant subtliss subtliss subtliss leavant subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss subtliss sub
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A; Molecule type: DNA
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C: Bron.; G: Rodlesch, C. C: Rodlesch, C. C: Rodlesch, C.; Erington, J.; Fabret, C.; Rorlesch, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fritz, C.; Fr
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A.Residues: 1-68 <SHI>
A.Cross-references: GB:M14202; NID:g143485; PIDN:AAA22725.1; PID:g143486
A.Cross-references: GB:M14202; NID:g143486; PIDN:AAA22725.1; PID:g143486
B.F.Fouet, A.; Arnaud, M.; Klier, A.; Rapoport, G.
Biochem. Biophys. Res. Commun. 119, 795-800, 1984
A.Title: Characterization of the precusor form of the exocellular levansucrase from A;Reference number: 139967; MUID:84178454
NYGGDDAFNIKSSFKLENNKKDRELAGLANGALGILKLTNNQSKPKVEEVYSPLVSTLMA 490-
                                                                                        CDEV----XXKLGDKYYLFSVTRVSRGSDRELTAKDNTIVGDNVAMIGYVSDSLMGKYKP
                                                                                                                                                                                                                                                                                                                                                                                         547 LNNSGVVLTASVPANWRTATYSYYAVPVAGHPDQVLITSYMSNKDFASGEGNYATWAPSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A. Status: nucleic acid sequence not shown; translation not shown
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A;Tile: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H97118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             levansucrase [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: H97118
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.;
Baly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
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A; Cross-references: GB: AE001437; PIDN: AAK79739.1; PID:g1S024744; GSPDB:GN00168
A; Experimental source: Clostridium acetobutylicum ATCC824
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLDVWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPTGDNHIYLLYNKYGDNDFSHWRN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 QFNASTLKNIASAKGYD-KNGNLIDLDVWDSWPLQNG-DGTVANYHGYHIVFALAGDPKN 121
                                                                                                                                                                                                                                                                    372 GFHYQTYEQFAN-GKDRENDDYCLRDPHVVQLENGDRYLVFEANTGTED-YQSDDQIYNW 429
                                                                                                                                                                                                                                                                                                                                                       430 ANYGGDDAFNIKSSFKLLNNKKDRELAGLANGALGILKLTNNQSKPKVEEVYSPLVSTLM 489
                                                                                                                                                                                                                                                                                                                                                                                                                                      323 IQLFFT-----SNDTSDYKLNDQRLATATLNLN-VDDNGVSIKSVDNYQVLFE-GD 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 VTDEIERANVFKMNGRWYLFTDSRGSKMTINGISSKD-----IYMLGFSSNSLTGPYK 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 AGSIFGTKETNVFQEWSGSAIVNDDGTIQLFFTSNDTSDYKLN--DQRLATATLNLNVDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 KGLAYNVEDALGSRQWAGSAILDENGMVQFFYTATGRKGEAVRTFEQRLVKTKFSINVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                490 ACDEV----XXKLGDKYYLFSVTRVSRGSDRELTAKDNTIVGDNVAMIGYVSDSLMGKYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLNNSGVVLTASVPANWRTATYSYYAVPVAGHPDQVLITSYMSNKDFASGEGNYATWAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDRENDDYCLRDPHVVQLENGDR-YLVFE
                                                                                                                                                                PTGDNHIYLLYNKYGDNDFSHWRNAGSIFGTKETNV------FQEWSGSAIVNDDGT
                                    -----YKETYGVSHITRYNMSKIPMEQNDLKFKVP
                                                                                 212 YSNAKEIKNMPATYTVDAQTGKMAHLDVWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.6%; Score 315; DB 2; 27.1%; Pred. No. 3.1e-10; Live 68; Mismatches 158.
161 IDAGSLTDDQINELNKINFSKSAEKGAKLTFKDLEGIGN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLLNIKGTKTSVISNSILQQGQLTIDN 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLVQINPDDTTTVLARATNQGDWVWDD
                       | :| :| | :| 16 ICSGIITQQTFASTNDMN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
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Best Local S
Matches 105
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J. Bacteriol. 183, 4823-4838, 2001
J. Bacteriol. 183, 4824-4838, 2001
A; Racteriol. 183, 4824-4838, 2001
A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Rocession: F97118
A; Ratus: preliminary
A; Molecule type: DNA
A; Residues: 1-489 < KUR>
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C; Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C; Date: 14-Sep-2011
R; Accession: F97118
R; Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gibson, J; Daly, M.J; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSDDQIYNWANYGGDDAFNIKSSFKLLNNKKDRELAGLANGALGILKLTNNQSRPKVEEV 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hexosyltransferase
                                                                                                                                                                                                                           144 NLKKLNPQAAKAVQNAKIDAGSLTDDQINELNKINFSKSAEKGAKLTFKDLEGIGNAIVK 203
                                                                                                                                                                                                                                                                                                          204 QD------PQYAIPYSNAKEIKNMPATYTVDAQTGKMAHLDVWDSWPVQDPVTGYV 253
                                                                                                                                                                                                                                                                                                                                                                                                                 -----QEWSGSAIVNDDGTIQLFFTSNDTSDYKLNDQRLATATLNLNVDDNGVSIKSVD 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NYQVLFEGDGFHYQTYEQFAN-GKDRENDDYCLRDPHVVQLENGDRYLVFEANTGTED-Y 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGEESLFNKAYYGKSTSFFRQESQKLLQSDKKR-TAELANGALGMIELNDDYT---LKKV 327
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                                                                                                                                                                                                                                                                                                                                                   49 HDMLQIPEQQKNEKYQVPEFDSSTIKNISSA-----KGLDVWDSWPLQN-ADGTV
                                                                                                                                                                                                                                                                                                                                                                                           SNYMGYQLVIAMMGIPNSPTGDNHIYLLYNKYGDNDFSHWRNAGSIFGTKETNVF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSPLVSTLMACDEV ---XXKLGDKYYLFSVTRVSRGSDRELTAKDNTIVGDNVAMIGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69;
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                                                                                                                                              Length 473;
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                                                                                                                                                                                     Indels
                     A;Gene: sacB
C;Keywords: extracellular protein; glycosyltransferase;
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-473/Product: levansucrase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 16.5%; Score 685.5; DB 2; Best Local Similarity 33.5%; Pred. No. 1.1e-30; Matches 170; Conservative 101; Mismatches 167;
                                                                                                                                          Query Match 18.0%; Score 746.5; DB 2; Best Local Similarity 36.3%; Pred. No. 4.2e-34; Matches 185; Conservative 92; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  levansucrase [imported] - Clostridium acetobutylicum
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    C;Genetics:
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Gaps

QY         528 DNVAMIGYVSDS-LMGKYKPLANSGVVLTASVPANWRTATYSYYAVPVAGHPDQVLITSY 586           Db         307GLYGFVSENGIFGFYEPLNGSGLVLGGPASQPTEAYAHYIMNNGLVESF 355           QY         587 MSINKDFASGEGNYATWAPSFLVQINPDDT 615           I         I	RESULT 7 S47527 S47527 Cypecies: Zymomonas mobilis C;Species: Zymomonas mobilis C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Mar-1999 C;Accession: S47527 R;Song, K. B.; Lee, S. K.; Joo, H.K.; Rhee, S. K. R;Song, K. B.; Lee, S. K.; Joo, H.K.; Rhee, S. K.	A;Title: Nucleotide and derived amino acid sequences of an extracellular sucrase gene A;Title: Nucleotide and derived amino acid sequences of an extracellular sucrase gene A;Reference number: S47527, MUID:94368848 A;Accession: S47527 A;Accession: S47527 A;Accession: S47527 A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-413 <son> A;Cross-references: EMBL:L08094</son>	Query Match 7.0%; Score 292; DB 2; Length 413; Best Local Similarity 26.3%; Pred. No. 5.6e-09; Matches 104; Conservative 69; Mismatches 153; Indels 70; Gaps 20; Qy 239 VWDSWPVQDPVTGVSNYMGYQLVIAMMIPNSPTGDNHIYLLYNKYGDNDFSHWRNAGS 298	Qy         299 IFGTKETNVFOEWSGSAIVNDDGTIQLFFTSNDTSDYKLNDQRLATATLNLNVDD 353           :	QY 413 ANTGTEDYQSDDQIYNMANYGGDDAFNIKSSFKLLNNKKDRELAGLANGALGILKLTNNQ 472	528 307 587 587 356	RESULT 8 JC2519 Levansucrase (EC 2.4.1.10) precursor - Zymomonas mobilis N;Alternate names: sucrose 6-fructosyltransferase C;Species: Zymomonas mobilis C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Jun-2000	C; Accession: JC2519; PC2376 R; Kyono, K.; Yanase, H.; Tonomura, K.; Kawasaki, H.; Sakai, T. R; Kyono, K.; Yanase, H.; Tonomura, K.; Kawasaki, H.; Sakai, T. Biosci. Biotechnol. Blochem. 59, 289-293, 1995 A; Title: Cloning and characterization of Zymomonas mobilis genes encoding extracellul A; Reference number: JC2519; MUID:95218269 A; Accession: JC2519 A; Molecule type: DNA A; Residues: 1-423 < KYO>
QY 413 ANTGTE-DYQSDDQIYNWANYGGDDAFNIKSSFKLLNNKKDRELAGLANGALGIL 466  Db 240 GNKGGKIEKMKPENIGDKLFRKNHIAPRGVENF-NGNVGIAVAQNK 284  QY 467 KLTNNQSKPKVEEVXSPLVSTLMACDEVXXKLGDKYYLFSVTRVSRGSDRELTAKDN 523  Db 285 DLTRFKLLPPLLEAVGVNQQLERPQIVMK-KNKYYLFTISHKFTYAQGLNGVD- 336	QY         524 TIVGDNVAMIGYVSDSLMGKYKPLNNSGVVLTASVPANRTRATYSYYAVPVAGHDDQVLI 583           Db         337GLYGFCGNSLRSNYKPLNGNGLVITNPTNDPYQTYSWYLVSGHDVLSFI 385           QY         584 TSYMSNKDPASGEGNYATWAPSFLVQI 610           Db         386 NEYHFNGQLRYGGTFAPTLQISL 408	RESULT 6 JC2520  beta-fructofuranosidase (EC 3.2.1.26) - Zymomonas mobilis N;Alternate names: invertase C;Species: Zymomonas mobilis C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Jun-2000 C;Accession: JC2520; PC2377; S50037	RiKyono, K.; Yanase, H.; Tonomura, K.; Kawasaki, H.; Sakai, T. Biosci. Blosci. Blotechnol. Blochem. 59, 289-293, 1995 A.Title: Cloning and Characterization of Zymomonas mobilis genes encoding extracellular A; Reference number: JC2519; MUID:95218269 A; Accession: JC2520 A; Molecule type: DNA A; Molecule type	A/Accession: PCJ3/(4) A/Molecule type: protein A/Molecule type: protein A/Residues: 1-21 <ky2> R/Rhee, S.K. Submitted to the EMBL Data Library, March 1994 A/Reference number: S50037 A/Status: preliminary A/Status: preliminary</ky2>	A.Residues: 1-104, S., 106-107, Tr, 109-413 <rhe> A.Residues: 1-104, S., 106-107, Tr, 109-413 <rhe> A.Cross-references: EMBL:L08094; NID:g468429; PIDN:AAA61488.1; PID:g468430 C.Genett.cs A.Genett.cs A.Genet.cs C.Keywords: glycosidase; hydrolase</rhe></rhe>	Query Match 7.4%; Score 308; DB 2; Length 413; Best Local Similarity 26.5%; Pred. No. 7.3e-10; Matches 105; Conservative 72; Mismatches 149; Indels 70; Ga 239 VWDSWPVQDPVTGYVSNYMGYQLVIAMGIPNSPTGDNHIYLLYNKYGDNDFSHWRNAGS 1 :  : : : : : : : : : : : : : : : : :	OY 299 IFCTKETUNEGEWGGSAIVNDDGTIQLEFTSNDTSDYKLNDORLATATLLLNVDD 353  101 LLQELANSRTAEWSGGTIMAPGSRNQVETEFTSTLFDKNGVREAVAAVTKGRIYADS 157  OY 354 NGVSIKSVDNYQVLEGDGFTVATVETFTSTLFDKNGVREAVAAVTKGRIYADS 157  OY 354 NGVSIKSVDNYQVLEGDGFTVATVETFTSTLFDKNGVREAPHV-VQLENGDRYLVFE 412	413 473 253

A:Cross-references: DDBJ:D17524; NID:g809529; PIDN:BAA04475.1; PID:g809530 A:Accession: PC2376 A:Molecula type: protein A:Residues: 1-19 <kxt2-< th=""><th>QY 228 DAQTGKMAHLDVWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPN 270  </th></kxt2-<>	QY 228 DAQTGKMAHLDVWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPN 270
C;Genetics: A;Gene: suc2E2 C;Reywords: glycosyltransferase; hexosyltransferase F:1-19/70main: signal sequence setatus predicted core	OY 271 SPTGDNHIYLLYNKYGDNDFSHWRNAGSIFGTKETNVFQEWSGSAIVNDDGTIQLFFT 328
3-423/Product: levansucrase #status predicted <mat></mat>	Qy 329 S-NDTSDYKLNDQRLATATLNLNVDDNGVSIKSVDNYQVLFBGDGFHYQTYEQFANGKDR 387 
Query Match 6.0%; Score 249.5; DB 2; Length 423; Best Local Similarity 23.8%; Pred. No. 1.3e-06; Matches 120; Conservative 67; Mismatches 150; Indels 167; Gaps 27;	388 ENDDYCLRDPHV-VQLENGDRYLVFEANTGTEDYQSDDQIYNWANYGGDDAFNIKSSFKL
QY 228 DAQTGKNAHLDVWDSNPVQDPVTGYVSNYMGYQLVIAMMGIPN 270	
OY 271 SPIGDNHIYLLYNKYGDNDFSHWRNAGSIFGTKETNVFQEWSGSAIVNDDGTIQLFFT 328	DD 232 PPKTETPDGAKYCAAAIGIAQALNEARTEWKLLPPLVTAFGVNDQTERPHVVFQNG- 287 QY 501 KYXLFSVTRVSRGSDRELTAKDNTIVGDNVAMIGYVSDS-LMGKYRPLNNSGVVLTASVP 559
OY 329 S-NDTSDYKLNDQRLATATLNLNVDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDR 387	Db 288 LTYLFTISHHSTYAD-GLSGPDGVYGFVSENGIFGPYEPLNGSGLVLGNP 336 Qy 560 ANWRTATYSYXAVPVAGHPDQVLITSYMSNKDFASGEGNYATWAPSFLVOINPDDT 615
OSDDQIYNW 42	FIDT IPSSDPNYRRYGGTLAPTIK NMLGVLKEGAANSAALPGEWGKPVDW
430 ANYGGDDAFN-IKSSFKLLNNKKDRELAGLANGALANGALGILKLTNNOSKPKVEE 47	Db 389 FVTEVKGYGYIPPQIEWLAEDESSNSAAALSLLNK 423
480	RESULT 10 S39195 Ievansucrase - Erwinia amylovora C.Species: Erwinia amylovora C.Spite: 06-Jan-1965 #sequence revision 06-Tan-1905 #taxt chance 08-041-1909
Qy 540 -LMGKYKPLNNSGVVLTASVPANWRTATYSYYAVPVACHPDQVLITSYMSNKDFASGEGN 598	ence of the levansiic
QY 599 YATWAPSFLVQINPDDTTTVLARATNQGDWVWDDSSRNDNMLGVLK 644	
Oy 645 EGAANSAALPGEWGKPVDWSLINR 668  1:	A;Residues: 1-415 <gei> A;Cross-references: EMBL:X75079; NID:g433558; PIDN:CAA52972.1; PID:g433559</gei>
RESULT 9	Query Match 5.7%; Score 236.5; DB 2; Length 415; Best Local Similarity 23.4%; Pred. No. 6.8e-06; Matches 96; Conservative 67; Mismatches 152; Indels 95; Gaps 20;
levansucrase - Zymomonas mobilis (ATCC 10988) C;Species: Zymomonas mobilis C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000 C;Accession: S33771	QY 239 VWDSRPVQDEVTGYVSNYMGYQLVIAMMGIPNSPTGDNHI 278
R; Song, K.B.; Joo, H.K.; Rhee, S.K. Blochim. Biophys. Acta 1173, 320-324, 1993 A; Title: Nucleotide sequence of levansucrase gene (levU) of Zymomonas mobilis ZMI (ATCCI A; Reference number: S33771: MUTD:93305726	QY 279 YLLYNKYGDNDFSHWRNAGSIFGTKETNVFQEWSGSAI-VNDDGTIQLFFTSNDTSDYKL 337  1::
A; Accession: S33771 A; Status: preliminary A; Molecule type: DNA A: Doct diagrams	QY 338 NDQRLATATLNLNVDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDRENDDYCLRDP 397 1
A;Cross-references: GB:L08093; NID:95880348; PIDN:AAA27695.1; PID:9295699	Qy 398 H-VVQLENGDRYLVFEANTGTEDYQSDDQIYNWANYGGDDAFNIKSSFKLLNNKKD 452
5.8%;	SINVAGPRÉSHEITQAEMGNUPPGYEDVGGAKY FINNGK DEVUFFUNGE UVGFT MAGNETAVY V FOR VITE GOVERN
~	253

Db 522 N	Query Match   4.94;   Score 203.5;   DB 2;   Length 4936;   Matches   Local Similarity   20.44;   Pred. No. 0.018  277;   Gaps   45;
Oy 509 RVSRGSDRELTAKDNTIVGDNVAMIGYVSDSLMGKYKPLANNSGVVLTASVPANMRTATYS 568  1	Dest Match

OY 324 QLEFTSNDTSDYKLANDQRLATATLALANDDNGVS 357	Qy 608 VQINPDDTTTVLARATNQGDWVWDDSSRN 636  :	J. Gen. Microbiol. 137, 2577-2593, 1991 A,Title: Molecular characterization of a cluster of at least two glucosyltransferase A; Reference number: A44811; MUID:92148377 A; Reference number: A44811; MUID:92148377 A; Rocession: S28810 A; Molecule type: DNA A; Residues: 1-51 <gif>A; CGRence CS: EMBL:211873 C; Genetics: A; Gene: 9tfK C; Superfamily: cpl repeat homology C; Keywords: glycosyltransferase; hxxosyltransferase F; 1456-1475/Domain: cpl repeat homology <cpp></cpp></gif>	Query Match 4.8%; Score 198.5; DB 2; Length 1599; Best Local Similarity 19.6%; Pred. No. 0.0064; Matches 179; Conservative 109; Mismatches 304; Indels 323; Gaps 45;  QY 1 MYKVGKNWAVATLVSASILMGGVVTAH-ADQVESNNYNGVAEVNTERQANG 50 ::
QY         497 KLGDKYYLESVTRVSRGSDRELTAKDNTI-VGDNVAMIGYVSDSLMGKYRPLNNSG 551           bb         938 PAGANSVNFSITAVDDNLIELPRNYSIIASAPGFISGSDSGVGVIDNDA 985           CY         552 VVLTASVPANMRTATYSYYAVPVAGHPDQVLITSYMSNKDFASGEGNYATWAPSFLVQ 609           L	FESULT 13 Table 12 Table 13 Table 13 Table 13 Table 13 Table 14 Table 14 Table 15 Ta	Query Match Best Local Similarity 22.0%; Pred. No. 0.0035; Matches 166; Conservative 99; Mismatches 312; Indels 177; Gaps 39; Qy 12 TLVSASILMGGVVTAHADQVESNNYNGVAEVNT 44  ::   :	200 216 258 269 312 367

Indels 341; Gaps

Length 1093;

61 ANSNTT---SGSTNQESSATNNTEN-AVVNESKNTNNTENAVVNENKNTNNTENAV--- 112 |:: | || :| :| || || 63 PTVNSSLAASDSTTEEPAVVSNMENTAQVSSSTNILTTESSTVDTNSPTQSNQNSIAISL 122 -----VNE-----NKNTN----NTENDNSQLKLTNNEQPSAATQANLKKLNPQAAK 154 123 TKASRESSINEPASTIANETTTADVITATOAQ-TSDPTTSLSSESGGKPTNPSQSK 181 155 AVQ-----KGA 187

113

2 YKVGKNWAVATLVSASILMGGV-VTAHADQVESNNYNGVAEVNTERQANGQIGVDGKIIS 60 

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Ouery Match
4.7%; Score 195.5; DB 2;
Best Local Similarity 19.5%; Pred. No. 0.0054;
Matches 169; Conservative 122; Mismatches 236;

182 STEITNIQVTGAVDNNATGSAVFDGVNITLQGKDITDDNLLDDSGLHWSEQIQVIAIKGT 241

238 DV------WDSWPVQDPVTGYVS--NYMGYQLVIAMMGIPNSPTGDNHIYLLYNKYGD 287 

188 KLTFKDLEGIGNAIVKQDPQYAIPYSNAKEIKNMPATYTV-DAQTGKMAH-----L

237

148LNPQ 195 GSHKKNFAITTVNGQ 195 EGIGNAIVKQDPQY. 245 DGYLTADSWY 255 NYMGYQLVI. 293 NYMTKALSNGBETKI 288NDFS  353 QDKWNINSESPGKEE 321 GTIQLFFTSNDTSD 410 GGYE-FLLSNDDDN 367 LFEDGFHYQTYEQI 469DMLQLVSSYM 408 YLVFEANTG 1 :             525 LSIVHGLFREVTNK 433	GSHKKNFAITVNGOVLYFDENGALSSTSTYSFTQETTNLVTDFTKNNAAYDSTKASFELU 194  GSHKKNFAITVNGOVLYFDENGALSSTSTYSFTQETTNLVTDFTKNNAAYDSTKASFELV 244  EGIGNAIVKQDPQYAIPYSNAKEIKNMPATYTVDAQTGKMAHLDVWDSWPVQDPVTGYVS 254	NYMGYQL	321 GTIQLFFTSNDTSDYKLNDQRLATATLNLNVDDNGVSIKSVDNYQV 366   :           :	LUVEE	473 SKPKVEEVYSPLVSTLMACDEVXXKLGDKYYLFSVTRVSR 512    :	557 SVPANWRTATYSYXAVPVAGHPDQVL	
		255 NYMGYQLVIAMMGIPNSPTGDN- 	321 GTIQLFFTSNDTSDYKLNDQRI   :         :         :	400 LLVREANIGT	473 SKPKVEEVYSPLVSTLMACDEVXXKIGD :	557 SVPANWRTATYSYXAVPVAGHDDO	635 RNDNMLGVLKEGAAN 649 1:     :  854 ALEAGVIYEGFSN 866

B86748

ByPothetical protein ykbc [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001

C;Accession: B86748

B;Bolotin, A.; Whicker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1039 <STO>
A;Cross-references: GB:AE005176; PID:g12723930; PIDN:AAK05084.1; GSPDB:GN00146
C;Genetics:
A;Gene: ykbc

288 NDFSHWRNAGSIFGTKETNVFQEWSGSAIVNDDGTIQL----FFTS--NDTSDYKLNDQ 340 341 RLAT---ATLNLNVDDNGVSIKSVDNYQVL------FEGDGFHYQ-TYEQFANGKD 386 EDY------428 609 VSGVDYYYMAKNLGITVDQAKELYSDL---VVASTSLEKNPNDGFADYLAGVHYGGSDFG 665 551 477 666 SLLQKPLNALPNGLNYSSGTNYQFKEIVEKVSTVDLSHLGTSIASYNQNGLTGILGDGLA 725 GKYKPLNNSGVVLTASVPANWRTATY-----SYYAVPVAGHPDQVLITSYMSNK---D 591 -----LRDPHVV-----QLENGDRYLVFEANTGT 417 507 541 761 ------MIGYVSDSLM :|| ODYNLPIPTIKGFGFVNLTENDASKNNPVINLIYNHNLPTYYGNHNNNIYYQGTAYTPSF ---WANYGGDDAFNIKSSFKLLNNKKDRELA---GLANGALGIL-----KLTNNQSKPKV G-----EANNTKLMSUNDYAGVFGGISFF-----EANNTKLMSUSLIGD -----EEVYSPLVSTLMACDEVXXKLGDKY--YLFSV-----592 FASGEGNYATWAPSFLVQINPDDTTTVL 619 : | | : | : | : | VLTNMGNFTTKSGS--ADVNADMDAYIL 787 RENDDYC-----436 492 429 542 387 418 478 726 508 762 δ g ò QQ g οχ ŏ q οy g δ g Qγ Q οy g δ g

Search completed: September 26, 2002, 18:25:13 Job time: 92 sec

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203 KODPQYAIPYSNAKEIKNMPATYTVDAQTGKMAHLDVWDSWPVQDPVTGYVSNYMGYQLV 262
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1 WYKVGKNWAVATLVSASTLM......LYAGSLLALFGLAAIEKRHA 792
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PcTUS_COMB.pep:*
                                      Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-968-685A-10
                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                  231628 segs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maximum Match 100%
Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
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267
236.5
236.5
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179.5
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170.5
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167.5
167.5
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                              Sequence 4, A Sequence 4, A Sequence 2, A Sequence 10, Sequence 10, Sequence 10, Sequence 5, A Sequence 5, A Sequence 5, A
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        ALIGNMENTS
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2353
2353
2353
2314
1912
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11529
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Gaps
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US-08-870-827-3

Sequence 3, Application US/08870827

Fatent No. 5962297

APPLICANT: TSUSAKi et al.

TITLE OF INVENTION: POLYEEPTIDE HAVING -FRUCTOFURANOSIDASE

TITLE OF INVENTION: ACTIVITY

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                            COUNTRY: USE

21P: 2004

COMPUTER READABLE FORM:

MEDIUM TYPE: Eloppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/870,827

FILING DATE: 06-JUN-1997

CLASSIFICATION OF A3:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 19 170,630/1996

FILING DATE: 10-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, ROGET L.

REFERENCE/DOCKET NUMBER: 25,618

REFERENCE/DOCKET NUMBER: 25,618

REFERENCE/DOCKET NUMBER: TSUSAKI-2

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.7%; Score 649.5; DB 2; 37.8%; Pred. No. 7.3e-43;
                                                                                                                                                                                                             E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 37.89
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: peptide US-08-870-827-3
                                                                                                                                                                                                             ADDRESSEE: BROWD'STREET: 419 Seven
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                                                                                                                                                            314 SAIVNDDGTIQLFFTSNDTSDYKLN------DQRLATATLNLNVDDNG-VSIKSVDN 363
                                                                                                                                                                                                                           421 QSDDQIYNWANYGGDDAFNIKSSFKLLNNKKDRELAGLANGALGILKLTNNQSKPKVEEV 480
                                                                                                                                                                                                                                                                                          481 YSPLVSTLMACDEV----XXKLGDKYYLFSVTRVSRGSDRELTAKDNTIVGDNVAMIGYV 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 NYMGYQLVIAMMGIPNSPIGDNHIY----LLYNKYG------DNDFSHWRNAGSIFGTK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 ET-NVFQ------EWSGSAIVNDDGTIQLFFT-----SNDTSDYKLNDQRLATATLN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 LINVDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDRENDDYCLRDPHVVQ--LENGD 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 VKANKKGVILTGFNKVTDLLQADGTYYQTGAQ-----NEFFNFRDPFTFEDPAHPGE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 AIVKQDPQYAIPYSNAKEIKNMPATYTV----DAQTGKMAHLDVWDSWPVQDPVTGYVS 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 RYLVFEANTGTEDYQSDDQIYNWANYG---GD-----DAFNIKSSFKLLNNKKDRELAG 457
                                                                                                                                                                                                                                                                                                                                                          537 SDSLMGKYKPLNNSGVVLTASVPANWRTATYSYYAVPVAGHPD--QVLTTSYMSNKDF 592
                                                                                                                                                                                                                                                                                                                                                                         27 QNSPQFKVPQFNASAIKNIDSAKGYD-KSGNLIDLDVWDSWPLQN-ADGTAANYHGYHIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.4%; Score 267; DB 4; Length 578;
23.8%; Pred. No. 1.2e-12;
tive 82; Mismatches 196; Indels 118;
                              263 IAMMGIPNSPIGDNHIYLLYNKYGDNDFSHWRNAGSIFGTKETNV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ITO, Tetsuya
APPLICANT: FUUTTA, KOKI
APPLICANT: HARA, KOKI
APPLICANT: HARA, KOZO
APPLICANT: TONOZUKA, Takashi
APPLICANT: TONOZUKA, TOSSHIYUKI
TILE OF INVENTION: BETA-FRUCTOFURANOSIDASE GENE
FILE REFERENCE: 10749-0001-0
CURRENT APPLICATION NUMBER: US/09/503,172A
CURRENT PILING DATE: 1999-06-08
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 9
NUMBER OF SEQ ID NOS: 9
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09503172A Patent No. 6284510 GENERAL INFORMATION:
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Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Arthrobacter sp
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
US-09-503-172A-2
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LENGTH: 578
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formation of polyfructans (levans), plasmids containing
these sequences as well as a process for preparing
                                                                                                                ----VGLAKAKNKQLTE--WEFLPPILSANCVTDQTERPQIYFKDG-KSYLFTISHRGT 395
                                                                                                                                                                                                                                                                                     444 APDFNQHPGHFQAXSHYVMP--GGLVQSFIDTIGTHDDFVRG----GTLAPTVKMDIGVG 497
                                                                                                                                                                                                                                                      -----RTATYSYYAVPVAGHPDQVLITSYMSNKDFASGEGNYATWAPSFLVQI--N 611
458 LANGALGILKLTNNQSKPKVEEVYSPLVSTLMACD----EVXXKLGDKYYLFSVTR---
                                                                                                                                                            510 VSRGSDRELTAKDNTIVGDNVAMIGYVSDSLMGKYKPLN-NSGVVLTASVPANW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GEIDER, Klaus
APPLICANT: WILLMITZER, Lothar
TITLE OF INVENTION: DNA sequences which lead to the
                                                                                                                                                                                                                                                                                                                                                PDDTTTVLARA-TNQGDWVWDDSSRNDNMLGVLKEGAANS 650
                                                                                                                                                                                                                                                                                                                                                                                  498 GDPTKTAVDYSYGSEGLGGWADIPANKHLFTNGKFGVAVS 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
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1180 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/OB/381,936
FILING DATE: 09-FEB-1995
CLASSIPICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 02110
FILING DATE: 09-AUG-1993
PROR APPLICATION NUMBER: DE P42270618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Meilman, Edward A.
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: P/951-108
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08381936
Patent No. 5792923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gebhardt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 08-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (212) 382-0888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 236925,
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: Z
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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10036-8403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       509 RVSRGSDRELTAKDNTIVGDNVAMIGYVSDSLMGKYKPLNNSGVVLTASVPANWRTATYS 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 -----HKYTFADNLTGPDGV--YGFVSDKLTGPYTPMNSSGLVL--GNPSSQPFQTYS 353
                                                                                                                                                                                                                                                                                                                                                                                                                                         44 IWDIMPLED-FDGEIISVNGWCIIFTLIADRNTDNPQFQDENGNYDIIRDWEDRHGRARI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279 YLLYNKYGDNDFSHWRNAGSIFGTKETNVFQEWSGSAI-VNDDGTIQLFFTSNDTSDYKL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fructosyltransferase Enzyme, Method
For its Production and DNA Encoding the Enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 NDQRLATATLNLNVDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDRENDDYCLRDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             453 RELAGLANGALGILKLINNQSKPKVEEVYSPLVSTLMACDEVXXK----LGDKYYLFSVT
                                                                                                                                                                                                                                                                                                                                                        95;
                                                                                                                                                                                                                                                                                                           Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :| :| | | :| : : | 354 HYVMP-----NGLVTSFIDSVPWKGKDYRIG----GTEAPTVKILLKGD 393
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                569 YYAVPVAGHPDQVLITSYMSN-----KDFASGEGNYATWAPSFLVQINPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 Mb
COMPUTER: IBM FOR Compariable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.0 for DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,232
FILING DATE: 22-December-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      5.7%; Score 236.5; DB 3;
23.4%; Pred. No. 1.7e-10;
tive 67; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                              239 VWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08362232
Patent No. 5641667
GENERAL INFORMATION:
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FILING DATE: 23-December-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 5
CORRESPONDENCES: S. ADDRESSES: HOffmann & Baron STREET: 350 Jericho Turnpike
                                                 TELERAX: (212) 382-0888
TELEX: 236925
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
           TELECOMMUNICATION INFORMATION:
                                   (212) 382-0700 (212) 382-0888
                                                                                                                                                                                                                                                                                                                              Best Local Similarity 23.48 Matches 96; Conservative
                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-943-374-2
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Jericho
                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                                           Query Match
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Patent No. 6028249

GENERAL INFORMATION:
GENERAL GENER, Manuela
APPLICANT: GEIDER, Klaus
APPLICANT: GEIDER, Klaus
APPLICANT: WILMITZER, Lothar
TITLE OF INVENTION: DNA sequences which lead to the
TITLE OF INVENTION: these sequences as well as a process for preparing
TITLE OF INVENTION: transgenic plants.
                                                      20;
                                                                                                                                44 INDIMPLED-FDGEIISVNGWCIIFTLTADRNTDNPQFQDENGNYDITRDWEDRHGRARI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 CYWYSRIGKD----WIFGGRVMAEGVAPTTREWAGTPILLNDRGDIDLYYTCVTPG---- 154
                                                                                                                                                                                                                                                                                                             398 H-VVQLENGDRYLVFEANT----GTEDYQSDDQIYNWANYGGDDAFNIKSSFKLLNNKKD 452
                                                                                                                                                                                                                                                                                                                                                                                                             205 SPFIDRNDGKLYMLFEGNVAGPRGSHEITQ-----AEMG-----NVPPGYEDVGGAKY 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 QA-----GCVG-LAVAKDLSGSE-WQILPPLITAVGVNDQTERPHFVFQDGKYYLFTIS 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  509 RVSRGSDRELTAKDNTIVGDNVAMIGYVSDSIMGKYKPLNNSGVVLTASVPANWRTATYS 568
                                                                                                                                                                                    279 YLLYNKYGDNDFSHWRNAGSIFGTKETNVFQEWSGSAI-VNDDGTIQLFFTSNDTSDYKL 337
                                                                                                                                                                                                                                                                          338 NDQRLATATLNINVDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDRENDDYCLRDP 397
                                                    95; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       453 RELAGLANGALGILKLINNQSKPKVEEVYSPLVSTLMACDEVXXK----LGDKYYLFSVT
       Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| :| | :|| : | : | | 354 HYVMP-----NGLVISFIDSVPWKGKDYRIG----GTEAPTVKILLKGD 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          569 YYAVPVAGHPDQVLITSYMSN-----KDFASGEGNYATWAPSFLVQINPD 613
                                                    Indels
Query Match 5.7%; Score 236.5; DB 1; Best Local Similarity 23.4%; Pred. No. 1.7e-10; Matches 96; Conservative 67; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                          239 VWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 180 Avenue of the Americas CITY: New York STATE: NY COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meilman, Edward A.
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: P/951-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/943,374
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FILING DATE: 08-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/381,936
FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036-8403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: DNA TITLE OF INVENTION: for TITLE OF INVENTION: the TITLE OF INVENTION: tra NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
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United States of America
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502 RADVNIAGFIOD 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 AD-----LGFRPUDP-NAETLQEVLDSGAYYQKANIGLA-----IATDSTLSKWK---F 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 LSPLISANCVNDQTERPQVYLHNGKYYFTISHRTTFAAGVD------GPD-GVY 393
                                                                                                                                                                                                                                                                                                                                                                                                                                220 NMPATYTVDAQTGKMAHLD--VWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPTG--D 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 RHVHARIGFFYRRAGIPASRRPVNGGWTYGGHLFPDGASAQVYAGQTYTNQ-AEWSGSSR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 EGDGFHYQTYEQFANGKDRENDDYCLRDPHVVQ--LENGDRYLVFEANT----GTEDYQS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               423 DDQIYNWANYGGDDAFNIKSSFKLLNNKKDRELA--GLANGALGILKLTNNQSKPKVEEV 480
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                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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For its Production and DNA Encoding the Enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 QPDGVLYQ-----NG--AQNEFFNFRDPFTFEDPKHPGVNYMVFEGNTAGQRGVANCTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 YSPLVSTLMACDEVXXKL----GDKYYLFSV---TRVSRGSDRELTAKDNTIVGDNVAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       534 GYVSDSLMGKYKPLNNSGVVLTASVPANWRTA......TYSYYAVPVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    577 HPDQVLITSYMSNKDFASGEGNYATWAPSFLVQINPDDTTTVLARATNQGDWVWDD--SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 VND--DGTIQLFFT----SNDTSDYKLN-DQRLATATL-NLNVDDNGVSIKSVDNYQVLF
                                                                                                                                                                                                                                                                                                                                                  Query Match 4.7%; Score 197; DB 1; Length 543; Best Local Similarity 23.8%; Pred. No. 3.3e-07; Matches 117; Conservative 78; Mismatches 175; Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
   TILE OF INVENTION: Fructosyltrar
   TILE OF INVENTION: For its Produ
   NUMBER OF SEQUENCES: 5
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: HOffmann & Baron
   STREET: 350 Jericho Turnpike
              NAME: Baron, Ronald J.
REGISTRATION UNDBER: 29,281
REFERENCE/DOCKET NUMBER: 294-2
RELECOMMUNICATION INPORMATION:
TELECOMMUNICATION 1100 B22-3550
TELEFAX: (516) 822-3550
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
TYPE: amino acid
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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Patent No. 5731173
GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: prof
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                                                                                                                                                                                                                                                                         HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----YGDNDFSHWRNAGSIFGTKETNVFQEWSGSAI 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VND--DGTIQLFFT----SNDTSDYKLN-DQRLATATL-NLNVDDNGVSIKSVDNYQVLF 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGDGFHYQTYEQFANGKDRENDDYCLRDPHVVQ--LENGDRYLVFEANT----GTEDYQS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423 DDQIYNWANYGGDDAFNIKSSFKLLNNKKDRELA--GLANGALGILKLTNNQSKPKVEEV 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 LSPLISANCVNDQTERPQVYLHNGKYYIFTISHRTTFAAGVD------GPD-GVY 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYVSDSLMGKYKPLNNSGVVLTASVPANWRTA------TYSYYAVPVAG 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            577 HPDQVLITSYMSNKDFASGEGNYATWAPSFLVQINPDDTTTVLARATNQGDWVWDD--SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.7%; Score 197; DB 1; Length 543;
23.8%; Pred. No. 3.3e-07;
tive 78; Mismatches 175; Indels 122;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
SOFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.0 for DOS
                                                                                                                       CURRENT ADPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/814,196
FILING DATE: 10-MAR-1997
CLASSIFICATION 135
FROM APPLICATION DATA:

APPLICATION NUMBER: US 08/362,232
FILING DATE: 22-December-1994
FILING DATE: 22-December-1993
APPLICATION NUMBER: CU 125/93
FILING DATE: 33-December-1993
APPLICATION NUMBER: C1 125/93
REGISTATION NUMBER: 294-29
RECERENCE/DOCKET NUMBER: 294-29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3560
TELEFAX: (516) 822-3560
TELEFAX: (516) 822-3560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 NHIY----ELYNK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 23.8 Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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STRANDEDNESS: un)
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---KYEFKDLPKYDEGK 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 IQLFFTSNDTSDYKLNDQRLATATLNLNVDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 KNWAVATLVSASILMGGVVTAHADQVESNNYNGVAEVNTERQANGQIGVDGKIISANSNT 65
                                383 LPSGDYIL----KEIE-APRPYTFDKDK------EYPFTMKDTDNQGY--- 419
                                                                                                                                                                                                     -----KPTIYFKLYKQ------DDN-QNTTPVDKAEIKKLEDGTTKVTWSNLP 488
                                                                                                                                                                                                                                              383 NGKDRENDDYCLRDPHVVQLENGD--RYLVFEANTGTEDYQSDDQIYNWANYGGDDAFNI 440
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203 KODPQYAIPYSNAKEIKNMPATYTVDAQTGKMAHLDVWDSWPVQDPVTGYVSNYMGYQLV 262
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                                                                                                         ----END------KNGKAIKYLVKEVNAQGEDTTPEGYTKK------
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APPLICANT: Foster. Timothy J.
APPLICANT: McDevitt, Danhen L.
TITLE OF INVENTION: The S. aureus Fibrinogen Binding Protein Gene FILE REPERENCE: 05344.1050115.
CURRENT APPLICATION NUMBER: US/08/293,728D
CURRENT FILING DATE: 1994-08-22
NUMBER OF SEQ ID NOS: 20
SSETWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        733 -KDNQDGKRPEKVSVNLLADGEKVKTLDVTSETNW----
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US-08-293-728-2
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                                             APPLICANT: GUSS, Bengt
APPLICANT: GUSS, Bengt
APPLICANT: HOOK, Magnus
APPLICANT: LONSEON, Hans
APPLICANT: LINDERG, Martin
APPLICANT: SIGNAS, Christer
APPLICANT: SIGNAS, Christer
TITLE OF INVENTION: A COLLAGEN BINDING PROTEIN AS WELL AS TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCHWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,031A FILING DATE: 22-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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|-----DGSVVKDNQKEIEIIT----
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CITY: Alexandria
STATE: Vireir:
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20.7%; Pred. No. 2.8e.
tive 85; Mismatches
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APPLICATION DATA:
APPLICATION NUMBER: US 07/861,804
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00707
FILING DATE: 22-OCT-1991
PRIOR APPLICATION NUMBER: SE 9003374-7
FILING DATE: 22-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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COUNTRY: United States
ZIP: 22313-1404
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; MOLECULE TYPE: protein
US-08-447-031A-2
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MEDIUM TYPE: Floppy
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NVKFKLSKK---
                                                 US-08-447-031A-2
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--TSGSTNQESSATNNTENAV------VNESKNTNNT--ENAVVNE--NKNTNNTENA 111
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APPLICANT: Foster, Timothy J.
APPLICANT: McDevitt, Damien L.
TITLE OF INVERTION: The S. aureus Fibrinogen Binding Protein Gene FILE REFERENCE: 05344.105011 un 0504121,868
CURRENT APPLICATION NUMBER: 05/09/421,868
CURRENT FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 08/293,728
PRIOR FILING DATE: 1994-08-22
SOFTWARE: Patentin Ver. 2.0
                                                                         112 VVNENKNTNNTENDNSQLKLTNNEQPSAATQANLKKLNPQAAKAVQNAKIDAGSLTDDQI
                                                                                                                                                  NELNKINFSKSAEKGAKLTFKDLEGIGNAIVKQDPQYAIPYSNA-
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Patent No. 6177084
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LENGTH: 933
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APPLICANT: LOOSMOTE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038-860
CURRENT APPLICATION NUMBER: US/09/268,347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 ITNQLTNVTVGIDSGTTV-----YPHQ---AGYVKLNYGF-----SVPNSAVKGDT 274
                                                                                                                                                                                                    --TSGSTNQESSATNNTENAV------VNESKNTNNT--ENAVVNE--NKNTNNTENA 111
                                                                                                                           6 KNWAVATLVSASILMGGVVTAHADQVESNNYNGVAEVNTERQANGQIGVDGKIISANSNT 65
                                                                                                                                                                                                                                                                                                                                                     NELNKINFSKSAEKGAKLTFKDLEGIGNAIVKQDPQYAIPYSNA---------KE
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                                               4.2%; Score 173; DB 4; Length 933;
20.5%; Pred. No. 6.1e-05;
ive 90; Mismatches 273; Indels 264;
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Patent No. 6335182
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                                                                                           Conservative
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                                                                         Best_Local Sim
Matches 162;
JS-09-421-868-2
                                                     Query Match
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                                                                                                                                                                                                                                                                       5 GKNWAVATL-----VSASILMGGVVTAHADQVE-SNNYNGV--AEVNTERQANGQ 51
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                                                                                                                                                                                          4.2%; Score 173; DB 4; Length 1004;
llarity 20.6%; Pred. No. 6.9e-05;
Conservative 122; Mismatches 333; Indels 280;
                                                                                                                                                                                                                                                                                                                                                   IGVDGKIISANSNTTSGSTNQESSATNNTE----
                                                                                                 ; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-268-347-30
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
LENGTH: 1004
                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                191;
                                                                                                                                                                                              Query Match
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Matches 19
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1430 EDINTTIVEMEGONSVINNKNKENSSLLKGDEEDIVMVNLKKENNYNSVINNVDCRKKDM 1489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.2%; Score 173; DB 2; Length 2391;
20.3%; Pred. No. 0.00028;
tive 93; Mismatches 227; Indels 13:
                                                                                                                                                                                                           APPLICANT: Stewart, Thomas S
APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, Milliam J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 VNESKNTN--NTENAVVNE---NKN----TNNTENAVV-NENKNTNNT---
                                                                                                                                                                                                                                                                                                                                                             :: Nixon & Vanderhye PC
1100 No. 5849573th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patchetin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-701-1995
758 AKQLPQTGNKSGLAGLYAGSLLALFG 783
                                      936 ASQLPQ-----ASMPGKSMVSIAG 954
                                                                                                                                          Sequence 2, Application US/08446855A Patent No. 5849573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION UNUMBER: 29.009
REFERENCE/CDCKET NUMBER: 47-81
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2391 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELEPHONE: 703-6+0
703-816-4100
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Matches 115; Conserv
                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Virginia
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Arlington
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                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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US-08-169-927-2
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                                                                                                                                               1595 -------DEYNINVIMMICSNYNNASAFVIGKDRIDILEND--CIEKIMDHTKKKYN 1641
                                                                                                                                                                                                                                                     1642 RLNNRRSTNERMALMVNNEKESNHEKGHR-RNGLNKKNKE----KNMEKNKGKNKDKKNY 1696
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                                                                 1544 GNNKNM-DMYLSKEKSISNKNPGNSYYVVDSVY-----NNEYKINKMKELIDNENLN 1594
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                          291 SHWRNAGSIFGTKETNVFQEWSGSAIVNDDGTIQLFFTSNDTSDYKLNDQRLATATLNLN 350
                                                                                                                    351 VDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDR----ENDDYCLRD-----PHVV 400
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APPLICANT: Stewart et al.
TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
Patent No. 6183996
TITLE OF INVENTION: Synthetase II
                                                                                                                                                                                                                                                                                                     457 GLANGALGILKLINNQSKPKVEEVYSPLÝSTLMACDEVXXKLGDKYY----LFSVTRVS
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4.2%; Score 173; DB 4; Length 2391;
Best Local Similarity 20.3%; Pred. No. 0.00028;
Matches 115; Conservative 93; Mismatches 227; Indels 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT PEDLICATION NUMBER: US/09/150,741
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PL6380
EARLIER FILING DATE: 1992-12-16
EARLIER FILING DATE: 1993-12-02
EARLIER FILING DATE: 1993-12-05
EARLIER FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATCHING DATE: 1995-07-06
SOFTWARE: PATCHING DATE: 1995-07-06
SOFTWARE: PATCHING DATE: 1995-07-06
SOFTWARE: PATCHIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                               1743 QGNNDDL-SNDNYLSSEELNTDEYDDD 1768
                                                                                                                                                                                                                                                                                                                                                                                                  512 RGSDRELTAKDNTIVGDNVAMIGYVSD 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09150741 Patent No. 6183996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-150-741-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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TITLE OF INVENTION: Gene and Protein Applicable to the TITLE OF INVENTION: Preparation of Vaccines for Rickettsia prowazekii and TITLE OF INVENTION: Rickettsia typhi and the Detection of Both
                                                                                                                                                                                                                                                                                                                                                                                                                     1697 HYVNH-----KRNNEYNSNNIESKFNNYV------DDINKK----EYYEDENDIYYFTHSS 1742
                                                                                                                                                                                                                                                                                                               -----DGKNINDECKTYKKNKYKDMGLNNNIVDELSNGTSHSTNDHLYLDNFNTSDEEI 1543
                                                                                             291 SHWRNAGSIFGTKETNVFQEWSGSAIVNDDGTIQLFFTSNDTSDYKLNDQRLATATLNLN 350
                                                                                                                                                                 VDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDR----ENDDYCLRD-----PHVV 400
                                                                                                                                                                                                                                                                          QLEN----GDRYLVFEANTGTEDYQSDDQIYNWANYGGDDAFNIKSSFKLLNNKKDRELA 456
                                                                                                                                                                                                                                                                                                                                                                                   GLANGALGILKLINNQSKPKVEEVYSPLVSTLMACDEVXXKLGDKYY-----LFSVTRVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Counsel, Naval Medical R & D Command STREET: Bidg. 1, T-12, 8901 Wisconsin Ave. CITY: Bethesda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1743 QGNNDDL-SNDNYLSSEELNTDEYDDD 1768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/742,128
FILING DATE: 08/09/91
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              512 RGSDRELTAKDNTIVGDNVAMIGYVSD 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08169927 Patent No. 5783441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Spevack, A. David
REGISTRATION NUMBER: 24,743
REFERENCE/DOCKET NUMBER: 75,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Carl, Mitchell
APPLICANT: Dobson, Michael E.
APPLICANT: Ching, Wei Mei
APPLICANT: Dasch, Gregory A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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19.5%;
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TELEFAX: (301) 295-1022
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20889-5606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Counsel, 1
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	KEKQVFFTTDYNNLGSIIANNYTINDDYTLTTGGIAGTDERITLGSVNGNANV 1007  SFLVQINPDDTTTVLARATNQDWVWDDSSRNIGGANSAALPGE- 656   :			IYNWANYG 461    :	FEGDGFHYOTYEQFANGKDRENDDYCLRDPHYVQLENGDRYLVFEANTGTEDYQSDDQ 425	NDDGTIQLFFTSNDTSDYKLNDQRLATATLNLNVDDNGVSIKSVDNYQVL 367 	GSIFORWSGSALV 317 	YVSNYMGYQLVIAAMGIPNSPTGDNHIYLLYNKYGDNDFSHWRNA 296 	EGIGNAIVKQDPQYAIPYSNAKEIKNMPATYTVDAQTGKMAHLDVWDSWPVQD-PVTG 251 		-NDNSQLKLTNNEQPSAATGAN	ENAVVNENKHTNHT 123 ::         :   :	VDGKIISANSNTTSGSTNQESSATNTENAV 84 	VGKNWAVATLVSASILMGGVYTAHADQVESNNYNGVAEVNTERQANGQIG 53 	tive 117; Mismatches 366; Indels 342; Gaps 47;
245 245 252 252 252 252 252 252 252 252		ELTAKDNTIVGDNVAMIGYVSDSLM :	ALGILKLTNNQSKFKVEEVYSPI   :  : :   : GTPLDVLTIKSTVGNGTVDNFNAPI							GPVNQ		VNESKNTNNT :   TADSK			200; Conservative
	953 605 1008 657 11068 712 1119 768		462	426								ю	8		Matches

Sequence 9, Application US/09336447A

Sequence 9, Sequence 1, Sequ ISANSNITISGSTNQ------ESSATNNTENAVVNESKNTNNTENAVVNENKNTN 106 107 NTENAVVNENKNT------NNTENDNSQ---LKLTNNEQPSAATQANLKKLN-- 149 150 -----PQAAKAVQN--AKIDAGSLTDDQINELNKINFSK----SAEKGAKLTFKDLEGIGN 199 253 VSNYMGYQLVIAMM----GIPNSPTGDNHIYLLYNKYGDNDFSHWRNAGSIFG----- 301 -TKETNVFQEWSGSAIVNDDGTIQLFFTSNDTSDYKLNDQRLATATLNLN---VDDNGVS 357 358 IKSVDNYQVLFEGDGFHYQTYEQFANG-------KDRENDDYCLRDPHVVQ 401 490 DNNINNIYELAQOQDQHSSDIKTLKNNVEBGLLDLSGRLIDQKADLTKDIKTLKN----N 545 Gaps LENG-----YNWANYGGDDAFNIK 441 442 SS-----FKLLNNKKDRELAGLANGALGILKLTNNQSKPKVEEVYSPLVSTLMAC 491 492 DEVXXKLGDKY-----YLFSVTRVSRGSDRELTAKDNTIVGDNVAMIG------ 534 4 VGKNWAVATLVSASILMGGVVTAHADQVESNNYNGVÄEVNTERQANGQIGVDG-----KI 58 200 AIVKQDPQYAIPYSNAKEIKNM-PATYTVDAQTGKMA-----HLDVWDSWPVQDPVTGY Indels 239; Query Match
4.1%; Score 170.5; DB 4; Length 941;
Best Local Similarity 20.7%; Pred. No. 9.8e-05;
Matches 190; Conservative 108; Mismatches 380; Indels 239 ; TYPE: PRT ; ORGANISM: Moraxella catarrhalis US-09-336-447A-9 LENGTH: 941 59 302 402 a g ò q à ò ò g ò P ð g ò a

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535 ---YVSD-SLMGKYKPLNNSGVVLT-ASVPANWRTATYSYYAVPVAGHPDQVLITSYMSN 589
                                     704 QDQHSSDIKTLAKVSAANTDRIAKNKAEADASFETLTKNONTLIEGG---EALVEQNKAI 760
                                                                             590 KDFASGEGNYATWAPSFLVQINPDÖTTTVLARATNQGDWVWDDSSRNDNMLGVLKEGAAN 649
                                                                                                                                                          SAALPGEWGKPVDWSLINRSPGLG----LKPHQPVQPKIDQPDQ--QPSGQNTKN-VTPG 702
                                                                                                                                                                                                                                                                817 KQ------ELILQNDRLNQINETNNHQ--DQKIDQLGYALKEQCQHFNNRISAV
                                                                                                                                                                                                                                     703 NGDKPAGKATPDNTNIDPSAQPSGQNTNIDPSAQXSGQNTKNV-TPGNEKQGKNTDAKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Barenkamp, Stephen I.
APPLICANT: St. Geme III, Joseph W.
TITLE OF INVENTION: Haemophilus Adhesion Proteins
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: S11va, Robin M.
REGISTRATION NUMBER: 38,304
REERENCE/DOCKET NUMBER: A-61053/RFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,995
FILING DATE: 24-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08409995
Patent No. 5646259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino acids
                                                                                                                                                                                                                                                                                                                  762 PQTGNKSGLAGLYAGSL 778
                                                                                                                                                                                                                                                                                                                                             918 ----YKIGLSWSDAGGL 930
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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SOFTWARE: PatentI
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STRANDEDNESS: dou
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APPLICANT: Barenk
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Ouery Match 4.1%; Score 170; DB 1; Length 1098;
Best Local Similarity 20.3%; Pred. No. 0.00014;
Matches 178; Conservative 100; Mismatches 301; Indels 300; Gaps
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22 GVVTAHADQVESNNYNGVAEVNTERQANGQIGVDGKIISANSNTTSGSTN-QESSATNNT 80

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: :: : : : : | DGITVKYDAKVG--DGLKLDGDKIAADTTALTVNDGKNANNPKGKVADVASTDEKKLVTA 470
                                                                                           962 LDPNDQSKGKGVVIDNVANGDISATSTDAINGSQLYAVAKGVTNLAGO-VNNLEGKVNKV 1020
                                                             ----TQANLKKLNPQAAKAVQNAKIDAGSLTDDQINELNKINFSKSAEKGAKLTFKDLEG 196
                                                                                                                                                    IGNAIVKQDPQYAIPYSNAKEIKNMPATYTVDAQTGKMAHLDVWDSWPVQDPVTGYVSNY 256
                                                                                                                                                                                                                                        MGYQLVIAMMGIPNSPTGDNHIYLLYNKYG----DNDFSHWRNAGSIFGTKETNVFQEWS 312
                                                                                                                                                                                                                                                                         362
                                                                                                                                                                                                                                                                                                                                                           | :: | :: | :: | | 585 GQSVKNYVSGLKKFGDANFDPLISSADNLIKQNDDAYKGLT---NLDEKGIDKQTPVVAD 641
                                                                                                                                                                                                                                                                                                                                                                                                                      363 NYQVLFEGD--GFHYQTYEQFANGKDRENDDYCLRDPHVYQLE------NGDRY 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVFEANTGTEDYQSDDQIYNWANYGGDDAFNIKSSFKLLNNKKDRELAGLANGALGILKL 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   700 ITFELAKG-EVVKSNE------728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  469 TNNQSKPKVEEVYSPLVSTLMACDEVXXKLGDKYYLFSVTRVSRGSDRELTAKDNTIVGD 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GN 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       529 NVAMIGYVSDSLMGKYKPLNNSGVVLTASVPANWRTATYSYYAVPVAGHPDQVLITSYMS 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 754 TVA-----VADAGGKVVSVTDNTEATITNKGSGY----VTGNQ----VADAIA 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           589 NKDFASGÉGNYATWAPSFLVQINPDDTTTVLARAT----NQGDWVWDDSSRNDNMLGVLK 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      796 KSGFELGLADEADAKRAF-----DDKTKALSAGTTEIVNAHDKVRFANGLNTKVSAATV 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESTDAN------GDKVTTTFVKTDVELPLTQIYNTDANGKKITKVVKDGQTKWYELNA 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 902 DGTADMTKEVTLGNVDSDGKKVVKDNDGKWYHAKADGTADKTKGEVSNDKVSTDEKHVVS 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ::| |:| | | L-------YVRQEGANFT------YSLQDALTGLTSIT
                                                                                                                                                                                                                                                                                                                               313 GSAIVNDDGTIQLF-----FTSNDTSDYKLNDQRLATATLNLNVDDNGVSIKS---VD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         690 QPSGQNTKNVTPGNGDKPAGKATPDN-------
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Search completed: September 26, 2002, 18:24:27 Job time: 46 sec

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; Search time 61.92 Seconds (without alignments) 1420.711 Million cell updates/sec
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/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MYKVGKNWAVATLVSASILM......LYAGSLLALFGLAAIEKRHA 792
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

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	Description	Novel	Novel	Novel	Novel	Novel	Novel	Novel	Novel	Novel	Novel	Novel
CHINALES	ID		ABG07167	ABG05590	ABG11754	ABG21645	ABG22589	ABG04946	ABG28407	ABG04307	ABG23205	ABG25769
	DB	22	22	22	22	22	22	22	22	22	22	22
	Length	881	893	774	774	1027	736	789	789	527	789	823
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                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques of restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or a food supplement. (II) and its binding partners are useful in medical maging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical contractions in the private of a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical contractions in the private of a formations in the produce other types of data and products dependent on DNA and diagnostics, forensics, gene mapping, identification of mutations contractions cand to produce other types of data and products dependent on DNA and diagnostic amino acid sequences of the invention.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 TENA----VVNESKNTN--NTENAVVNENKNTNNTENAVVNENKN----TNNTENDNSQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 LKLTINNEQPSAATQANLKKLNPQAAKAVQNAKIDAGSLTDDQINELNKINFSKSAEKGAK 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           476 KVEEVYSPLVSTLMACDEV----XXKLGDKYYLFSVTRVSRGSDRELTAKDNTIVGDNVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
19.2%; Score 795.5; DB 22; Length
Best Local Similarity 34.2%; Pred. No. 4.2e-42;
Matches 217; Conservative 115; Mismatches 222; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences
                                     Claim 20; SEQ ID No 52010; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     881 AA;
biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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polypeptide (II) sequences. (I) is useful as hybridisation probes, and gone mapping, and in recombinant production of (II). The and gone mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polypucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques of restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and camino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3) chromosome mapping; gene mapping; gene therapy; forensic;
supplement; medical imaging; dlagnostic; genetic disorder.
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19.2%; Score 795.5; DB 22; Length
Best Local Similarity 34.2%; Pred. No. 4.2e-42;
Matches 217; Conservative 115; Mismatches 222; Indels
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                                 Claim 20; SEQ ID No 37526; 103pp; English.
592 FASGEGNYATWAPSFLVQINPDDTTTVLARATNQG
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249 VTGYVSNYMGYQLVIAMMGIPNSPTGDNHIYLLYNKYGDNDFSHWRNAGSIFGTKETNVF
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                                                                 LKLTNNEQPSAATQANLKKLNPQAAKAVQNAKIDAGSLTDDQINELNKINFSKSAEKGAK
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                                                                                                       LTFKDLEGIGNAIVKQDPQYAIPYSNAKEIKNMPATYTVDAQTGKMAHLDVWDSWPVODP
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food supplement; medical imaging; diagnostic; genetic disorder.
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2000US-0649167
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polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The inventor reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase and in recombinant production of (III). The polymerase are also used in diagnostics as expressed agenes. (I) is useful in gene therapy techniques for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or treat diseases states involving at polymeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating clisorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in clasorates, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and cannon acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in alectronic format directly from WIPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 QDPQYAIPYSNAKEIKNMPATYTVDAQTGKMAHLDVWDSWPVQDPVTGYVSNYMGYQLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 AMMGIPNSPTGDNHÌYLLYNKYGDNDFSHWRNAGSIFGTKETNVF------QEWS
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                                                                                                                                                                                                    invention relates to isolated polynucleotide (I) and
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PER) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PER) primers, oligomers, and for changes and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or treating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amno acid sequences of the invention.

Clagnostic amno acid sequences of the invention.

Clagnostic but was obtained in electronic format directly from WIPO
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                                                 144 NLKKLNPQAAKAVQNAKIDAGSLTDDQINELNKINFSKSAEKGAKLTFKDLEGIGNAIVK 203
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19.0%; Score 789.5; DB 22; Length 774; ilarity 34.3%; Pred. No. 8.4e-42; Conservative 100; Mismatches 220; Indels 105;
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                                                                                                                                                                                                                                                           Claim 20; SEQ ID No 52004; 103pp; English.
                                             Tang YT;
                                           Liu C,
                                                                                    WPI; 2001-639362/73
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymeratase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating clisorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cliagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and
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573 ylvfeantgtengyqgeeslfnkayygggtnffrkesqklqqsakkrd-aelangalgii 631
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                                        467 KLINNQSKPKVEEVYSPLVSTLMACDEV----XXKLGDKYYLFSVTRVSRGSDRELTAKD
                                                                  523 NTIVGDNVAMIGYVSDSLMGKYKPLNNSGVVLTASVPANWRTATYSYYAVPVAGHPDQVL
                                                                                                                                                                                                        583 ITSYMSNKDFASGEGNYATWAPSFLVQINPDDTTTVLARATNQGDWVWDDSSRNDNMLG-
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23-AUG-2000; 2000US-0649167.
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N-PSDB; AAS86776.
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amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                            TSGSTNQESSATNNTENA-----VVNESKNTNNTENAVVNENKNTNNTENA-----VVNE 115
                                                                                                                                               NKNTNNTENDNSQLKLTNNEQPSAATQANLKKLNPQAAKAVQNAKIDAGSLTDDQINELN 175
                                                                                                                                                                                KINFSKSAEKGAKLTFKDLEGIGNAIVKQDPQYAIPYSNAKEIKNMPATYTVDAQTGKMA 235
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                                                                                                                                                                                              HLDVWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPTGDNHIYLLYNKYGDNDFSHWRN
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food supplement; medical imaging; diagnostic; genetic disorder.
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686 nnvvitsymtnrgff--edkkatfapsflmnikgnktsvvknsilegg 731
                                                                                            98; Mismatches 215; Indels
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                                                                              DB 22;
                                                                           Score 773.5; DB 2 Pred. No. 8.1e-41;
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35.7%;
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Matches 210; Conservative
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapphig, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy *Lechniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical maging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in adjanostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other trails to assess biodiversity and to produce other types of data and products dependent on DNA and
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Note: The sequence data for this patent did not appear in the printed sepecification, but was obtained in electronic format directly from WI at ftp.wipo.int/pub/published_pct_sequences.
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36.3%; Pred. No. 4.5e-40;
iive 95; Mismatches 183
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30-MAR-2001; 2001WO-US08631
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2000US-0649167
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23-AUG-2000;
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443 SFKLLNNKKDRELAGLANGALGILKLTNNQSKPKVEEVYSPLVSTLMACDEV----XXKL 498

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Homo sapiens.
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Note: The sequence data for this patent did not appear in the printed
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GDKYYLFSVTRVSRGSDRELTAKDNTIVGDNVAMIGYVSDSLMGKYKPLNNSGVVLTASV
                                                    559 PANWRTATYSYYAVPVAGHPDQVLITSYMSNKDFASGEGNYATWAPSFLVQINPDDTTTV
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                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #28398.
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                                                                                                                                                   71;
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                                                                                                                                                 95; Mismatches
                                                                                                                Score 762.5;
Pred. No. 4.5
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36.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328 TSNDTSDYKLNDQRLATATLNLNVDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFAN-GKD 386
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                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                        Claim 20; SEQ ID No 34666; 103pp; English.
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23-AUG-2000; 2000US-0649167
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N-PSDB; AAS68494.
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                                    (HYSE-) HYSEQ INC.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerse chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding pariners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                YYLFSVTRVSRGSDRELTAKDNTIVGDNVAMIGYVSDSLMGKYKPLNNSGVVLTASVPAN 561
                                                                                                                                                                      562 WRTATYSYYAVPVAGHPDQVLITSYMSNKDFASGEGNYATWAPSFLVQINPDDTTTVLAR
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food supplement; medical imaging; diagnostic; genetic disorder.
                            Length 789;
                                               Mismatches 178; Indels
                            DB 22;
                           18.3%; Score 760.5; DB 36.1%; Pred. No. 6e-40;
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, conformers, and for chromosome and gene mapping, and in recombinant production of (II). The conformal and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques conformal activity of (II) or to treat disease states involving conformal activity of (II) or to treat disease states involving an following conformation of supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in cappositics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human conformation, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                      20; SEQ ID No 56128; 103pp; English.
Tang YT;
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Matches 197; Conservative
Drmanac RT, Liu C,
                                                                    WPI; 2001-639362/73.
N-PSDB; AAS89956.
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(HYSE-) HYSEQ INC
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Query Match
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                            562 WRTATYSYYAVPVAGHPDQVLITSYMSNKDFASGEGNYATWAPSFLVQINPDDTTTVLAR 621
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23-AUG-2000; 2000US-0649167.
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N-PSDB; AAS85834.
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                                                                 99 VNENKNTNNTENAVVNENKNTNNTENDNSQLKLTNNEQPSAATQANLKKLNPQAAKAVQN 158
                                                                                   38 tallaggatqafakennqkay-ketygvshitrhdmlqipkq--qqnekyqvpqfdqsti
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         Length 493;
                                    Indels
          DB 22;
18 3%; Score . 4.2e-...
36.1%; Pred. No. 4.2e-...
34; Mismatches 179;
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23-AUG-2000; 2000US-0649167.
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                        Best Local Similarity 36.1%
Matches 197; Conservative
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 KIISANSNTTSGSTNQESSATNNTENAVVNESKNTN-NTENAVVNENKNTNNTENAVVNE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 NKNTNNTENDNSQLKLTNNEQPSAATQANLKKLNPQAAKAVQNAKIDAGSLTDDQINELN 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 HLDVWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPTGDNHIYLLYNKYGDNDFSHWRN
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18.3%; Score 758; DB 22; Length 5.
Best Local Similarity 34.7%; Pred. No. 5.2e-40;
Matches 201; Conservative 106; Mismatches 199; Indels
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WPI; 2001-639362/73
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                      N-PSDB; AAS86019
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food supplement; medical imaging; diagnostic; genetic disorder.
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ilarity 34.7%; Pred. No. 5.4e-40;
Conservative 106; Mismatches 199
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N-PSDB; AAS85789.
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The invention relates to isolated polynucleotide (I) and polymerase chain reaction (PGR) primers, oligomers, and for chromosome polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymeristic and an expensed and in gene therapy techniques constituting activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving constituting antibodies against it, detecting or (II). (II) is useful for generating antibodies against it, detecting or a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating cisorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cresponsible for generic disorders or other trails to assess blodiversity and to produce other types of data and products dependent on DNA and cand to produce other types of data and products dependent on DNA and diagnostic amino acid sequences. Abg00010-Abg30377 represent novel human CC diagnostic amino acid sequence data for this patent did not appear in the printed conspectification, but was obtained in electronic format directly from WIPO at fitp.wipo.int/pub/published_pct_sequences.
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                 SEQ ID No 51961; 103pp; English
                                                                                                            biodiversity
                                                                                                                                                                           Claim 20;
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Length 1095; Indels Query Match
18.3%; Score 758; DB 22;
Best Local Similarity 34.7%; Pred. No. 1.3e-39;
Matches 201; Conservative 106; Mismatches 199;

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Sequence

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ALIGNMENTS

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203 KQDPQYAIPYSNAKEIKNMPATYTVDAQTGKMAHLDVWDSWPVQDPVTGYVSNYMGYQLV 262
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Sequence 3,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                        Compugen Ltd
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US-08-943-374-2
US-08-362-322-2
US-08-814-196-2
US-08-447-031A-2
US-08-421-868-2
US-09-421-868-2
US-09-268-347-30
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US-08-685-467-2
US-09-913-942-2
US-09-669-974-32
US-09-268-347-44
US-09-268-347-34
US-09-268-347-34
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US-08-968-685A-10
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US-08-169-927-2
US-09-336-447A-9
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               GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
                                                                                               protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                              -FRUCTOFURANOSIDASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 15.7%; Score 649.5; DB 2; Best Local Similarity 37.8%; Pred. No. 7.3e-43; Matches 158; Conservative 77; Mismatches 132;
                                     GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Tsusaki et al.
TITLE OF INVENTION: POLYPEPTIDE HAVING -FRUCT
TITLE OF INVENTION: ACTIVITY
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWNY AND MEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSUSAKI-2
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 3, Application US/08870827
Patent No. 5962297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25,618
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REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TS
TELECOMMUNICATION INFORMATION:
TELECHHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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26;
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                                                                                                                                                                                                                                                                     SAIVNDDGTIQLFFTSNDTSDYKLN------DQRLATATLNLNVDDNG-VSIKSVDN 363
                                                                                                                                                                                                 QSDDQIYNWANYGGDDAFNIKSSFKLLNNKKDRELAGLANGALGILKLTNNQSKPKVEEV 480
                                                                                                                                                                                                                                                                                                                  481 YSPLVSTLMACDEV----XXKLGDKYYLFSVTRVSRGSDRELTAKDNTIVGDNVAMIGYV 536
                                                                                                                                                                                                                                                                                                                                        126 -VNGWEIIFSLVADRNLGFDDRHVFAKIGYFYRPAGVPAAERPEN--GGWTYGGLVFKEG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 ET-NVFQ-----EWSGSAIVNDDGTIQLFFT-----SNDTSDYKLNDQRLATATLN 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 LNVDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDRENDDYCLRDPHVVQ--LENGD 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 AIVKQDPQYAIPYSNAKEIKNMPATYTV----DAQTGKMAHLDVWDSWPVQDPVTGYVS 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 NYMGYQLVIAMMGIPNSPTGDNHIY----LLYNKYG------DNDFSHWRNAGSIFGTK 303
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27 ONSPQFKVPQFNASAIKNIDSAKGYD-KSGNLIDLDVWDSWPLON-ADGTAANYHGYHIV 84
                                                                                                                                                                                                                                                                                                                                                                                         537 SDSLMGKYKPLNNSGVVLTASVPANWRTATYSYYAVPVAGHPD--QVLITSYMSNKDF 592
                                                                                                                                                                                                                                                                                                                                                                                                             6.4%; Score 267; DB 4; Length 578; '23.8%; Pred. No. 1.2e-12; tive 82; Mismatches 196; Indels 118;
                                  263 IAMMGIPNSPTGDNHIYLLYNKYGDNDFSHWRNAGSIFGTKETNV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: TO, TELSUYA
APPLICANT: HATA, KOKI
APPLICANT: HATA, KOKI
APPLICANT: HATA, KOKI
APPLICANT: TONOZUKA, Takashi
APPLICANT: SAKANO, YOShIYUKI
TITLE OF INVENTION: BETA-FRUCTOFURANOSIDASE GENE
FILE REFERENCE: 10749-0001-0
CURRENT APPLICATION NUMBER: US/09/503,172A
CURRENT FILING DATE: 2000-02-14
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09503172A
Patent No. 6284510
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Best Local Similarity 23.8°
Matches 124; Conservative
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APPLICANT: GEIDER, Klaus
APPLICANT: WILLMITZER, Lothar
TITLE OF INVENTION: DNA sequences which lead to the
TITLE OF INVENTION: formation of polyfructans (levans), plasmids containing
TITLE OF INVENTION: these sequences as well as a process for preparing
TITLE OF INVENTION: transgenic plants.
                                                                                                                                                                                                                                           -----RTATYSYYAVPVAGHPDQVLITSYMSNKDFASGEGNYATWAPSFLVQI--N 611
                                                              458 LANGALGILKLTNNQSKPKVEEVYSPLVSTLMACD----EVXXKLGDKYYLFSVTR--- 509
                                                                                                                                                                                                                                                                                       444 APDFNQHPGHFQAYSHYVMP--GGLVQSFIDTIGTHDDFVRG----GTLAPTVKMDIGVG 497
                                                                                                          ----VGLAKAKNKQLTE--WEFLPPILSANCVTDQTERPQIYFKDG-KSYLFTISHRGT
                                                                                                                                                                               510 VSRGSDRELTAKDNTIVGDNVAMIGYVSDSLMGKYKPLN-NSGVVLTASVPANW----
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,936
FILING DATE: 09-FEB-1995
                                                                                                                                                                                                                                                                                                                              612 PDDTTTVLARA-TNQGDWVWDDSSRNDNMLGVLKEGAANS 650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEE: Ostrolenk, Faber, Gerb & Soffen : 1180 Avenue of the Americas New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION: 900
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 02110
FILING DATE: 09-A0G-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P42270618
FILING DATE: 08-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meilman, Edward A.
REGISTRATION NUMBER: 24,735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P/951-108
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 382-0700
TELEPA: (212) 382-0808
TELEX: (212) 382-0808
TELEX: 236925
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08381936
Patent No. 5792923
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Gebhardt
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; MOLECULE TYPE: protein
US-08-381-936-2
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GEIER, G
GEIDER,
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APPLICANT:
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305 -----HKYTFADNLTGPDGV--YGFVSDKLTGPYTPMNSSGLVL--GNPSSQPFQTYS 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 YLLYNKYGDNDFSHWRNAGSIFGTKETNVFQEWSGSAI-VNDDGTIQLFFTSNDTSDYKL 337
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For its Production and DNA Encoding the Enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 NDQRLATATLNLNVDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDRENDDYCLRDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398 H-VVQLENGDRYLVFEANT----GTEDYQSDDQIYNWANYGGDDAFNIKSSFKLLNNKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      453 RELAGLANGALGILKLINNQSKPKVEEVYSPLVSTLMACDEVXXK----LGDKYYLFSVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 CYWYSRTGKD----WIFGGRVMAEGVAPTTREWAGTPILLNDRGDIDLYYTCVTPG---
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                                                                                                                                                                                                                                                                                            Length 415;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| :| | | | | : | | : | | 354 HYVMP-----NGLVTSFIDSVPWKGKDYRIG----GTEAPTVKILLKGD 393
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                         5.7%; Score 236.5; DB 3;
3.4%; Pred. No. 1.7e-10;
ve 67; Mismatches 152;
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MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PROSYMS-DOS
SOFTWARE: Wordperfect 6.0 for DOS
                                                                                                                                                                                                                                                                                                                                                                                    239 VWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPT-----
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APPLICATION NUMBER: US/08/362,232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08362232
Patent No. 5641667
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 22-December-1994 PRIOR APPLICATION DATA:
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350 Jericho Turnpike
TELECOMMUNICATION INFORMATION
              TELEPHONE: (212) 382-0700
TELEFAX: (212) 382-0888
TELEKX: 236925
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      23.4%;
                                                                                                                                   LENGTH: 415 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                 Ouery Match 5.7%
Best Local Similarity 23.4%
Matches 96; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-943-374-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
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CITY: Jericho
STATE: New York
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ZIP: 11758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        formation of polyfructans (levans), plasmids containing these sequences as well as a process for preparing transgenic plants.
                                               20;
                                                                                                                                                                                                                                                                                                                                                                                                   --ATIAKVRGKIVTSDQSVSLEGFQQVTSLFSADGTIYQTEEQ-----NAFWNFRDP 204
                                                                                                                                                                                                                                                                                                                                                                      H-VVQLENGDRYLVFEANT----GTEDYQSDDQIYNWANYGGDDAFNIKSSFKLLNNKKD 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           509 RVSRGSDRELTAKDNTIVGDNVAMIGYVSDSLMGKYKPLNNSGVVLTASVPANWRTATYS 568
                                                                                             -GDNHI 278
                                                                                                                                                                                     279 YLLYNKYGDNDFSHWRNAGSIFGTKETNVFQEWSGSAI-VNDDGTIQLFFTSNDTSDYKL 337
                                               95; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RELAGLANGALGILKLTNNQSKPKVEEVYSPLVSTLMACDEVXXK----LGDKYYLFSVT
                                                                                                                                                                                                                                                                             338 NDQRLATATLNLNVDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDRENDDYCLRDP
       Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  569 YYAVPVAGHPDQVLITSYMSN-----KDFASGEGNYATWAPSFLVQINPD 613
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                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: ROBER, Manuela
APPLICANT: GEIER, Gebhardt
APPLICANT: GEIER, Klaus
APPLICANT: WILLMITZER, Lothar
ITILE OF INVENTION: DAs sequences which lead to the
ITILE OF INVENTION: Tormation of polyfructans (levans),
ITILE OF INVENTION: these sequences as well as a proces;
ITILE OF INVENTION: transgenic plants.
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPRRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,374
  Query Match 5.7%; Score 236.5; DB 1; Best Local Similarity 23.4%; Pred. No. 1.7e-10; Matches 96; Conservative 67; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ostrolenk, Faber, Gerb & Soffen
                                                                                               239 VWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1180 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Mellman, Edward A. REGISTRATION NUMBER: 24,735 REFERENCE/DOCKET NUMBER: P/951-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P42270618
FILING DATE: 08-DEC-1992
ATTORREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/381,936
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Patent No. 6028249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036-8403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-943-374-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 LSPLISANCVNDQTERPQVYLHNGKYYIFTISHRTTFAAGVD-------GPD-GVY 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPDQVLITSYMSNKDFASGEGNYATWAPSFLVQINPDDTTTVLARATNQGDWVWDD--SS 634
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                                                                                                                                                                                                                                                                                                                                                                    4.7%; Score 197; DB 1; Length 543;
23.8%; Pred. No. 3.3e-07;
htive 78; Mismatches 175; Indels 122; Gaps.
                                                                                                                                                                                                                                                                                                                                                                                                                                                220 NMPATYTVDAQTGKMAHLD--VWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPTG--D 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 NIPADFPV-----INPDVWVWDTWTLIDKHADQFS-YNGWEVIFCLTADPNAGYGFDD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 NHIY----LLYNK-----YGDNDFSHWRNAGSIFGTKETNVFQEWSGSAI 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 VND--DGTIQLFFT----SNDTSDYKLN-DQRLATATL-NLNVDDNGVSIKSVDNYQVLF 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Fructosyltransferase Enzyme, Method
TITLE OF INVENTION: For its Production and DNA Encoding the Enzyme.
WUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Hoffmann & Baron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TYSYYAVPVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 YSPLVSTLMACDEVXXKL----GDKYYLFSV---TRVSRGSDRELTAKONTIVGDNVAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYVSDSLMGKYKPLNNSGVVLTASVPANWRTA---
MAME: MATON, ROBALD J. REGISTRATION NUMBER: 29,281
REFERENCE/DOCKET NUMBER: 294-29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3ec.
NFORMATON
                                                                                              INFORMATION:

(516) 822-3550
TELEFAX: (516) 822-3550
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
TYPE: amino acid
STRANDEDNESS: unknormation acids
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08814196 Patent No. 5731173 GENERAL INFORMATION:
APPLICANT:
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350 Jericho Turnpike
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Best Local Similarity 23.8%
Matches 117; Conservative
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RADVNIAGFIQD 513
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STREET: 350 c
ormy: Jericho
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; MOLECULE TYPE: F
; HYPOTHETICAL: NC
US-08-362-232-2
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STATE:
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249 QPDGVLYQ-----NG--AQNEFFNFRDPFTFEDPKHPGVNYWVFEGNTAGQRGVANCTE 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 VND--DGTIQLFFT----SNDTSDYKLN-DQRLATATL-NLNVDDNGVSIKSVDNYQVLF 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 EGDGFHYQTYEQFANGKDRENDDYCLRDPHVVQ--LENGDRYLVFEANT----GTEDYQS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 423 DDQIYNWANYGGDDAFNIKSSFKLLNNKKDRELA--GLANGALGILKLTNNQSKPKVEEV 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 RHVHARIGFFYRRAGIPASRRPVNGGWTYGGHLFPDGASAQVYAGQTYTNQ-AEWSGSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         534 GYVSDSLMGKYKPLNNSGVVLTASVPANWRTA-------TYSYYAVPVAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 GFVGDGIRSDFQPM-NYGSGLTMGNPTDLNTAAGTDFDPSPDQNPRAFQSYSHYVMPGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.7%; Score 197; DB 1; Length 543;
23.8%; Pred. No. 3.3e-07;
Live 78; Mismatches 175; Indels 122;
                ZIP: 11758
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Wordperfect 6.0 for DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/362,232
FILING DATE: 22-December-1994
APPLICATION NUMBER: CU 125/93
FILING DATE: 23-December-1993
ATTORNEY/AGENT INFORMATION:
United States of America
                                                                                                                                                                                                APPLICATION NUMBER: US/08/814,196
FILING DATE: 10-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         543 amino acids
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Best Local Similarity 23.8%
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Baron, Ronald J. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-814-196-2
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502 RADVNIAGFIQD 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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-----KPIIYFKLYKQ------DDN-QNTTPVDKAEIKKLEDGTIKVTWSNLP 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --KYEFKDLPKYDEGK 780
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                                                                                                                                                                                                                                                                                                                                                                 441 KSSFKLLNNKKDRELAGLANGALGILKLTNNQSKPKVEEVYSPL-----VSTLMACDEV 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 KNWAVATLVSASILMGGVVTAHADQVESNNYNGVAEVNTERQANGQIGVDGKIISANSNT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 KODPOYAIPYSNAKEIKNMPATYTVDAQTGKMAHLDVWDSWPVQDPVTGYVSNYMGYQLV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08293728D

Sequence 2, Application US/08293728D

Sequence 2, Application US/08293728D

GENERAL INFORMATION:

APPLICANT: POSTER: Timothy J.

APPLICANT: BOSTER: Timothy J.

TITLE OF INVENTION: The S. aureus Fibrinogen Binding Protein Gene;

FILE REFERENCE: 05344.105011

CURRENT PAPLICATION NUMBER: US/08/293,728D

CURRENT FILING DAIE: 1994-08-22

NUMBER OF SEQ ID NOS: 20

SEQ ID NO 2

LENGTH: 933
                                                                                                                                                                                                                                                                                                                                                                                                495 XXKLGDKYYLFSVTRVSRGSDRELTAKDNTIVGDNVAMIGYVSD----SLMGKYKPLNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         551 GVVLTASVPANWRTATYSYYAVPVAGHPDQVLITSYMSNKDFASGE-----GNYA-TW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----OGDWVWDDSS
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                                                                                                                        323 IQLFFTSNDTSDYKLNDQRLATATLNLNVDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         635 RNDNMLGVLKEGAANSAALPGEWGKPVD-----WSLINRSPGLGLKPHQPVQPKIDQP-
                                                                                        263 IAMMGIPNSPTGDNHIYLLYNKYGDNDFSHWRNAGSIFGTKETNVFQEWSGSAIVNDDGT
                                           ----EYPFTMKDTDNQGY---
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4.2%; Score 173; DB 3; L
Best Local Similarity '20.5%; Pred. No. 6.1e-05;
Matches 162; Conservative 90; Mismatches 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       733 -KDNQDGKRPEKVSVNLLADGEKVKTLDVTSETNW----
                                    LPSGDYIL-----KEIE-APRPYTFDKDK------
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CORGANISM: Staphylococcus aureus
US-08-293-728-2
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                                                                                                                                      APPLICANT: GUSS, Bengt
APPLICANT: GUSS, Bengt
APPLICANT: HOOK, Magnus
APPLICANT: JUNDSENG, Martin
APPLICANT: JUNDSENG, Martin
APPLICANT: SIGNAS, Christer
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APPLICANT: SIGNAS, Christer
APPLICANT: SIGNAS, Christer
APPLICANT: JOHNES WELL AS
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.3%; Score 179.5; DB 2;
20.7%; Pred. No. 2.8e-05;
Live 85; Mismatches 294;
                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/861,804
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00707
FILING DATE: 22-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9003374-7
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FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
                                                                   Sequence 2, Application US/08447031A Patent No. 5851794 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39,300
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REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (703) 836-5620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 22-OCT-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1183 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 20.7
Matches 167; Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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US-08-447-031A-2
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                                                -08-447-031A-2
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US-09-421-868-2

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                                                                                                                                                                                231
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--TSGSTNQESSATNNTENAV-----VNESKNTNNT--ENAVVNE--NKNTNNTENA 111
                                                                                                     ATTOSSNTNAEELVNO----TSNETTFNDTNTVSSVNSPONSTNAENV----STTODTS 179
                                                                                                                                                                                                                  IKNMPATYTVDAQTGKMAHLDVWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPT-GDN
                                                                                                                                                                                                                                                      ITNOLTNVTVGIDSGTTV----YPHQ---AGYVKLNYGF-----SVPNSAVKGDT
                                                                                                                                                                                                                                                                                           HIYLLYNKYGDNDFSHWRNAGSIFGTKETNVFQEWSGSAIVNDDGTIQLFFTSNDTSDYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               430 NTSIKVYKVDNAAD----LSESYFVNPENFEDVTNSVNITFPNPNQYKVEFNTPDDQITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LARATNQGDWVWDDSSRNDNMLGVLKEGAANSAALPGEWGKPVDWS---LINRSPGLGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYIVVVNGH--IDPNSKGDLALRSTLYG-YNSNII---W-RSMSWDNEVAFNNGSGSGDG
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                                                                                                                                                                    ----GNVTLATGIGSTTANKTVLVDYEKYG--------KFYNLSI----
                                DDTNVSDTKTSSNTNNGETSVAQNPAQQETTQSSSTNATTEETPVTGEATTTTTNQANTP
                                                                      112 VVNENKNTNNTENDNSQLKLTNNEQPSAATQANLKKLNPQAAKAVQNAKIDAGSLTDDQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Foster, Timothy J.
APPLICANT: McDevitt, Damien L.
TITLE OF INVENTION: The S. aureus Fibrinogen Binding Protein Gene FILE REFERENCE: 05344.105011
CURRENT APPLICATION NUMBER: 05/09/421,868
CURRENT FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 08/293,728
PRIOR FILING DATE: 1994-08-22
                                                                                                                                           172 NELNKINFSKSAEKGAKLTFKDLEGIGNAIVKQDPQYAIPYSNA
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ORGANISM: Staphylococcus aureus
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SOFTWARE: PatentIn Ve
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LENGTH: 933
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Score 173; DB 4; Length 933;
Pred. No. 6.1e-05;
); Mismatches 273; Indels 264;
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   4.2%;
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4.2%; Score 173; DB 4; Length 1004;
Best Local Similarity 20.6%; Pred. No. 6.9e-05;
Matches 191; Conservative 122; Mismatches 333; Indels 280;
                                                                                                                                                                                                                                                                                                                             52 IGVDGKIISANSNTTSGSTNQESSATNNTE------
                                                                                   ; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-268-347-30
CURRENT FILING DATE: 1999-03-16
             NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
                                                                    LENGTH: 1004
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1382 GKEEKSIGSDDTNILSAQNSNNNFSCNNENMNKAN------VDVNVLEND-TKKR 1429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.2%; Score 173; DB 2; Length 2391;
20.3%; Pred. No. 0.00028;
.ive 93; Mismatches 227; Indels 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 VNESKNTN--NTENAVVNE---NKN----TNNTENAVV-NENKNTNNT-----
                                                                                                                                                                                                                APPLICANT: Stewart, Thomas S
APPLICANT: Flores, Maria V
APPLICANT: 0'Sullivan, William J
IITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                        E: Nixon & Vanderhye PC
1100 No. 5849573th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUREENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-Jul-1995
758 AKQLPQTGNKSGLAGLYAGSLLALFG 783
                             936 ASQLPQ-----ASMPGKSMVSIAG 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                      Sequence 2, Application US/08446855A Patent No. 5849573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNALIA DE LEGITA CONTROL DE RECISTRATION NUMBER: 29.009
REGISTRATION NUMBER: 47-80
REFERENCE/DOCKET NUMBER: 47-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2391 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: linear
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Arlington STATE: Virginia
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                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                           US-08-446-855A-2
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                        1275 VKNHLYNEVVD-DKDTQLH------KENNNNNNNNSGNVENKCKLNKESYGYNNSSNCI 1326
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291 SHWRNAGSIFGTKETNVFQEWSGSAIVNDDGTIQLFFTSNDTSDYKLNDQRLATATLNLN 350
                                                                                                                                                                                    401 QLEN----GDRYLVFEANTGTEDYQSDDQIYNWANYGGDDAFNIKSSFKLLNNKKDRELA 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 VESNNYNGVAEVNTERQANGQIGVDGKIISANSNTTSGST-----NQESSATNNTENAV 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Stewart et al.
TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
Patent No. 6183996
TITLE OF INVENTION: Synthetase II
FILE REFERENCE:
                                                                                      351 VDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDR----ENDDYCLRD-----PHVV
                                                                                                                                                                                                                                                                             457 GLANGALGILKLTNNQSKPKVEEVYSPLVSTLMACDEVXXKLGDKYY-----LFSVTRVS
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20.3%; Pred. No. 0.00028;
Live 93; Mismatches 227; Indels 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: protein US-09-150-741-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/150,741
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PL6380
EARLIER FILING DATE: 1992-12-16
EARLIER FILING DATE: 1993-12-02
EARLIER APPLICATION NUMBER: AU93/00617
EARLIER APPLICATION NUMBER: 08446,855
EARLIER FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                   1743 QGNNDDL-SNDNYLSSEELNTDEYDDD 1768
                                                                                                                                                                                                                                                                                                                                                                          512 RGSDRELTAKDNTIVGDNVAMIGYVSD 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09150741 Patent No. 6183996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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Best Local Similarity 20.3%
Matches 115; Conservative
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LENGTH: 2391
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GENERAL INFORMATION:
APPLICANT: Carl, Mitchell
APPLICANT: Dobson, Michael E.
APPLICANT: Ching, Wel Mel
APPLICANT: Ching, Wel Mel
APPLICANT: Ching, Wel Mel
APPLICANT: Ching, Wel Mel
APPLICANT: Dasch, Gregory A
TITLE OF INVENTION: Gene and Protein Applicable to the
TITLE OF INVENTION: Preparation of Vaccines for Rickettsia prowazekii and
TITLE OF INVENTION: Rickettsia typhi and the Detection of Both
-----DGKNINDECKTYKKNKYKDMGLNNNIVDELSNGTSHSTNDHLYLDNFNTSDEEI 1543
                                                                                       1544 GNNKNM-DMYLSKEKSISNKNPGNSYYVVDSVY-----NNEYKINKMKELIDNENLN 1594
                                                                                                                                                                                   ------DEYNNNVMMNCSNYNNASAFVNGKDRNDNLEND--CIEKNMDHTYKHYN 1641
                                                                                                                                                                                                                                                                                                                                                                      1697 HYVNH-----KRNNEXNSNNIESKFNNYV-----DDINKK---EYYEDENDIYYFTHSS 1742
                                                                                                                                                                                                                                  401 QLEN----GDRYLVFEANTGTEDYQSDDQIYNWANYGGDDAFNIKSSFKLLNNKKDRELA 456
                                            291 SHWRNAGSIFGTKETNVFQEWSGSAIVNDDGTIQLFFTSNDTSDYKLNDQRLATATLNLN 350
                                                                                                                                                                                                                                                                                                                                 457 GLANGALGILKLINNQSKPKVEEVYSPLVSTLMACDEVXXKLGDKYY----LFSVTRVS
                                                                                                                                        351 VDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDR----ENDDYCLRD-----PHVV
                                                                                                                                                                                                                                                                                 1642 RLNNRRSTNERMMLMVNNEKESNHEKGHR-RNGLNKKNKE----KNMEKNKGKNKDKKNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Counsel, Naval Medical R & D Command
Bldg. 1, T-12, 8901 Wisconsin Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NATA:
APPLICATION NUMBER: US/08/169,927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 172; DB 1;
Pred. No. 0.00018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           512 RGSDRELTAKDNTIVGDNVAMIGYVSD 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/742,128
FILING DATE: 08/09/91
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08169927
Patent No. 5783441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Spevack, A. David
RECISTRATION NUMBER: 24,743
REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.18;
19.58;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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20889-5606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bethesda
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US-08-169-927-2
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US-08-169-927-2
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200; Conservative 117; Mismatches 366; Indels 342; Gaps	VGKNWAVATLVSASILMGGVVTAHADQVESNNYNGVAEVNTERQANGQIG 53	VSKNGA-ATEFNVTGTLGGNLKGIIELNTAAVAGKLISLGGAANAVIG 291	VDGKIISANSNTTSGSTNOESSAT-;NNTENAV 84	ŢNN	TADSKVIITENSNFGSTNFGNLDTQIVVPDTKILKGNFIGDVKNNGNTAGVIT 404	-NDNSQLKLTNNEQPSAATQAN 144		GPVNQNALMNNNALAAGSIQLDGSAIITGDIGNGGVNAALQHITLANDASKILALDGANI 524	EGIGNAIVKQDPQYAIPYSNAKEIKNMPATYTVDAQTGKMAHLDVWDSWPVQD-PVTG 251 	YVSNYMGYQLVIAMMGIPNSPTGDNHIYLLYNKYGDNDFSHWRNA 296	SIGTVVANTKTLAQLNIGSSKTILNAGDVAINELVIENNGSVQLNHNTYLITKTINAANQ 642		GQIIVAADPLNTNTTLADGTNLGSAENPLSTIHFATKAANADSILNVGKGVNLYANNITT 702	NDOCTIQLEFTSNDTSDYKLNDORLATATLALANDANGVSIKSVDNYQVL 367	RYI.VFEANTGTENYOSDDO	79	IYNWANYG	ITVTLNKQGAYFGVLKQVIISGPGNIVFNEIGNVGIVHGIAANSISFENASLGTSLFLPS 850	ALGILKLTNNQSKPKVEEVYSPLVSTLMACDEVXXKLGDKYYLFSVTRVSRGSDR 516	GTPLDVLTIKSTVGNGTVDNFNAPIV-VVSGIDSMINNGQIIGBKKNIIALSLGSDN 906	ELTAKDNTIVGDNVAMIGYVSDSLMCKYKPLNNSG-VVLTASVPAN 561 :              SITVNANTLKS	SYYAVPVAGHPDOVI.TTSYMSNKDF		SFLVQINPDDTTTVLARATNGGDWVWDDSSRNDNMLGVLKEGAANSAALPGE- 656	:	WGKPVDWSLINRSPGLGLKPHQPVQPKIDQPDQQPSGQNTKNVTPGNGDKPAGKA 711	YSQNIDEGTYNLTILNSNVILG-GGTTAINGEIDLLTNNLIFANGTSTWGDN 1118	TPDNTNIDPSAQPSGQNTNIDPSAQXSGQNTKNVTPGNEKQGKNTDAKQLPQTGNK- 767   :  :     :     : TSISTTLNVSSGNIGQVVIAEDAQVNATTTGTTTIKIQDNANANFSGTQAYTLIQGGARF 1178	SGLAG 772	:
Matches	4	245	54	85	352	124	145	465	195	252	583	297	643	318			426	791	462	851	517	562		909	1008		1068	712	768	1179
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APPLICANT: HANSEN, ERIC J.
APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: COPE, LESLIE D.
APPLICANT: PISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
CURRENT PREDENBURG, ROSS A.
TITLE OF INVENTION: USPAI AND USPAZ ANTIGENS OF MORAXELLA CATARHALIS
FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 9
LENGTH: 941 59 ISANSNTTSGSTNQ------ESSATNNTENAVVNESKNTNNTENAVVNENKNTN 106 156 IGNNSTVVGGSNNQAKGEHSTIAGGKNNQATGNGSFAAGVENKADAN--NAVALGNKNTI 213 107 NTENAVVNENKNT------NNTENDNSQ----LKLTNNEQPSAATQANLKKLN-- 149 214 EGTNSVAIGSNNTVKTGKENVFILGSNTNTENAQSGSVLLGNNTAGKAATTVNNAEVNGL 273 | : | | : | | : | | : | | 3.74 TLENFAGASKANANNIGTUSVGS----ENNERQIVNVGAGQISATSTDAVNGSQLHALAK 329 -----PQAAKAVQN--AKIDAGSLTDDQINELNKINFSK---SAEKGAKLTFKDLEGIGN 199 :: | : : | : | | : | | 377 KADIKGLNKEVKELDKEVKLSRDIGS-----LHDDVADNQDSIAKNKADIKGLNKEVKE 431 358 IKSVDNYQVLFEGDGFHYQTYEQFANG-------KDRENDDYCLRDPHVVQ 401 402 LENG-----YNWANYGGDDAFNIK 441 546 VEEGLLDLSGRLIDQKADIAKNQADIAQNQTDIQDLAAYNELQDQYAQKQTEAIDALNKA 605 253 VSNYMGYQLVIAMM ---- GIPNSPTGDNHIYLLYNKYGDNDFSHWRNAGSIFG----- 301 302 -TKETNVFQEWSGSALVNDDGTIQLFFTSNDTSDYKLNDQRLATATLNLN---VDDNGVS 357 Query Match 4.1%; Score 170.5; DB 4; Length 941;
Best Local Similarity 20.7%; Pred. No. 9.8e-05;
Matches 190; Conservative 108; Mismatches 380; Indels 239; Gaps SS-----FKLLNNKKDRELAGLANGALGILKLTNNQSKPKVEEVYSPLVSTLMAC 491 4 VGKNWAVATLVSASILMGGVVTAHADQVESNNYNGVAEVNTERQANGQIGVDG----KI 58 AIVKQDPQYAIPYSNAKEIKNM-PATYTVDAQTGKMA-----HLDVWDSWPVQDPVTGY 490 DNNINNIYELAQQQDQHSSDIKTLKNNVEEGLLDLSGRLIDQRADLTKDIKTLKN----N DEVXXKLGDKY----YLFSVTRVSRGSDRELTAKDNT IVGDNVAMIG-------Sequence 9, Application US/09336447A Patent No. 6310190 GENERAL INFORMATION: ORGANISM: Moraxella catarrhalis US-09-336-447A-9 -09-336-447A-9 150 200 909 492 644 442 q g à ò g á qq ò Ω ŏ QQ ŏ q δ qq Óγ QQ δλ a

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                                                                                                                                     161 NOELEGFAAHADVODKOILONQADITINKTAIEONINRTVANGFEIEKNKAGI----ATN 816
                                                                                                                                                                                   SAALPGEWGKPVDWSLINRSPGLG - . . . LKPHQPVQPKIDQPDQ - . QPSGQNTKN - VTPG 702
                                                                                                                                                                                                                              817 KQ------ELILQNDRLNQINETNNHQ--DQKIDQLGYALKEQGQHFNNRISAV 862
                                                                                                                                                                                                                                                                                                         535 ---YVSD-SLMGKYKPLNNSGVVLT-ASVPANWRTATYSYYAVPVAGHPDQVLITSYMSN 589
                                                                                           590 KDFASGEGNYATWAPSFLVQINPDDTTTVLARATNQGDWVWDDSSRNDNMLGVLKEGAAN 649
                                                                                                                                                                                                                                                                            703 NGDKPAGKATPDNTNIDPSAQPSGQNTNIDPSAQXSGQNTKNV-TPGNEKQGKNTDAKQL 761
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                             Indels 300;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,995 FILING DATE: 24-MAR-1995 CLASSIFICATION:
ATORNEY/AGENT INFORMATION:
NAME: S11va; RODIN M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A 61053/RFT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Barenkamp, Stephen I.
APPLICANT: St. Geme III, Joseph W.
TILE OF INVENTION: Haemophilus Adhesion Proteins
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08409995 Patent No. 5646259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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STATE: CA
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                                                                                                                                                                                                     313 GSAIVNDDGTIQLF-----FTSNDTSDYKLNDQRLATATLNLNVDDNGVSIKS---VD 362
                                                                                                                                                                                                                                                                                                                  363 NYQVLFEGD--GFHYQTYEQFANGKDRENDDYCLRDPHVVQLE-------NGDRY 408
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                                                                                                              IGNAIVKQDPQYAIPYSNAKEIKNMPATYTVDAQTGKMAHLDVWDSWPVQDPVTGYVSNY 256
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Submitted (JAN-1998)
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             64 QFNASTLKNIASAKGYD-KNGNLIDLDVWDSWPLQNG-DGTVANYHGYHIVFALAGDPKN 121
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212 YSNAKEIKNMPATYTVDAQTGKMAHLDVWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNS 271
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Bezzate S., Aymerich S., Chambert R., Czarnes S., Berge O., Heulin T Fistuption of the Paenibacillus polymyxa levansucrase gene impairs its ability to aggregate soil in the wheat rhizosphere."; Environ. Microbiol. 2:333-342(2000).

EMBL: AJ13737; CAB39377.1; -
InterPro; IPR003469; Glyco_hydro_68.

Pfam; PF02435; Glyco_hydro_68; 1.

SEQUENCE 499 AA; 55317 MW; E646CD986292336C CRC64;
                                                         278 IYLLYNKYGDNDFSHWRNAGSIFGTKE------TNVFQEWSGSAIVNDDGTIQLFFT
                                                                                                                                                                                                                                    ACDEV----XXKLGDKYYLFSVTRVSRGSDRELTAKDNTIVGDNVAMIGYVSDSLMGKYK
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Bacteria: Firmicutes; Bacillus/Cloštridium group;
Bacillus/Staphylococcus group; Paenibacillus.
NCBI_TaxID=1406;
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Sp. V30.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB010272; BAA32083.1; -.
EMBL; AB010272; BAA32083.1; -.
EMBL; AB010275; GJYco_hydro_68.
Pfam; PF02435; GJYco_hydro_68.1.
SEQUENCE 487.AA; 53412 MW; 7F52A47921824AE3 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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No. 2.4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84; Mismatches 141;
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                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325; Pubmed-11466586;

Medling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol., 183:4833,4838(2001).
316 IVNDDGTIQLFFTSNDTSDYKLN------DQRLATATLNLNVDDNG-VSIKSVDNYQ 365
                                                                                                                                          291
                                                                                                                                                                                   DDQIYNWANYGGDDAFNIKSSFKLLNNKKDRELAGLANGALGILKLTNNQSKPKVEEVYS 482
                                                                                                                                                                                                                                                                                PLVSTLMACDEV----XXKLGDKYYLFSVTRVSRGSDRELTAKDNTIVGDNVAMIGYVSD 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 GGVHITNCSKHQVILEPDGVXYQTMQQ-AKGP----IIXSFRDPYFFEDPKTKKDYLIFE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 AGSIFGTKETNVFQEWSGSAIVNDDGTIQLFFTSNDTSDYKLN--DQRLATATLNLNVDD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 NGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDRENDDYCLRDPHVVQLENGDR-YLVFE 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 413 ANTGTE-DYQSDDQIYNWANYGGDDAFNIKSSFKLLNNKKDRELAGLANGALGIL----- 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLDVWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPTGDNHIYLLYNKYGDNDFSHWRN 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                         VLFE-GDGFHYQTYEQFAN-GKDRENDDYCLRDPHVVQLENGDRYLVFEANTGTED-YQS
                                                                                                                    539 SLMGKYKPLNNSGVVLTASVPANWRTATYSYYAVPVAGHPD--QVLITSYMSNKDF 592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.6%; Score 315; DB 16; Length 428; 27.1%; Pred. No. 3e-08; Live 68; Mismatches 158; Indels 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9670B154B178E23E CRC64;
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Last sequence update)
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Pfam; PF02435; 'Glyco_hydro_68; 1.
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SEQUENCE 428 AA
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192 KDLEGIGNAIVKQDPQYAIPYSNAKEIKN-MPATYTVDAQTGKMAHLDVWDSWPVQDPVT 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFRDPFTFRDONNPSDPTEYMVFEGNSA ---FVREQQXVDAARAGQNTTLATCTEEDLG 412
KLTNNQSKPKVEEVYSPLVSTLMACDEVXXKLGDKYYLFSVTR----VSRGSDRELTAKDN 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QAAGGAAAQDANGFKADNPGWANATKHTGAAHG-----VEENYTAKWTRADAMQIQRVF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 QP-QGAVRAPTRLPEQLIMP-----EISNGFPAT-----SEDVWVWDTWTLTDEAA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATSKPYDPRIVQSEGRIYATKNGVVLTGFRTQHQLLVPDGKYYQTREQ------NPGV 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 SATNNTENAVVNESKNTNNTENAVVNENKNTNNTENAVVNENKNTNNTENDSQLKLTNN 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQP--SAATQAN-LKKLNPQAAKAVQNAKIDAGSLTDDQINELNKINESKSAEKGAKLTF 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                  26 AGTGTTALADETPSPTPSSSATAEASPEAGADQKNDQSPADQGQATQTPTDQGQAGQADQ
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                                                                                                          TIVGDNVAMIGYVSDSLMGKYKPLNNSGVVLTASVPANWRTATYSYYAVPVAGHPDQVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bergeron L.J., Morou-Bermudez E., Burne R.A.; "Characterization of the fructosyltransferase gene of Actinomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G-----TKETNVF--QEWSGSAIVNDDGTIQLFFTS------NDTSDY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Actinomycineae; Actinomycetaceae; Actinomyces. NCBL_TaxID=1655;
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR228582; ARG09737.1;
InterPro; IRR003469; Glyco, hydro_68.
Pfam; PF02435; Glyco_hydro_68; 1.
Transferase.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                     630
                                                                                                                                                                                                                     584 TSYMSNKDFASGEGNYATWAPSFLVQI 610
                                                                                                                                                                                                                                                       386 NEYHFNGQLRYG----GTFAPTLQISL 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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SEQUENCE FROM N.A.
STRAIN-ATCC 12104, WVU45;
                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinomyces naeslundii.
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01-DEC-2001
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31;

449 NKK---DRELAGLANGALGILKLTN----NQSKPKVE-EVYSPLVSTLMACDEVXXK-- 497

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Pseudomonas.
NCBI_TaxID=318;
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364 MP-
                                                                  Q93TM1
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--LGDKYYLFSVTRVSRGSDRELTAKDNTIVGDNVAMIGYVSDSLMGKYKPLN-NSGVVL 554
                                          279 YLLYNKYGDNDFSHWRNAGSIFGTKETNVFQEWSGSAI-VNDDGTIQLFFT--SNDTSDY 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLNDQRLATATLNLNVDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDRENDDYCLR 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 DPHVVQLENGDRYLVFEANTGTEDYQSDDQIYNWANYGGDDAFNIKSSFKLLNNKKDREL 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|| : |: |: |: -FQTACVGIAVARDEDGDD--WEMLPPLLTAVGVNDQTERPHFVFQDGKYYLFTISHT- 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   512 RGSDRELTAKDNTIVGDNVAMIGYVSDSLMGKKRPLNNSGVVLTASVPANWRTATYSYYA 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                555 TASVPANWRIA------TYSYYAVPVAGHPDQVLITSYMSNKDFASGEGNY
                                                                                                                            580 GSLSPTVKLNIS-GDTTSV------DRTYGINGLGGFADIPADRARTNGGATR
                                                                                   600 ATWAPSFLVQINPDDTTTVLARATNQGDWVWDDSSRNDNMLGVLKEGAANSAALPGEWGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           456 AGLANGALGILKLTNNQSKPKVEEVYSPLVSTLMACDEVXXK----LGDKYYLFSVTRVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           572 VPVAGHPDQVLITSYM-----SNKDFASGEGNYATWAPSFLVQINPDDTTTV 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91;
                                                                                                                                                                                                                                                                                               Pseudomonas aurantiaca.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Length 424;
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                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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22.9%; Pred. No. 0.00018;
tive 76; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 VWDSWPVQDPVTGYVSNYMGYQLVIAMMG--IPNSPT----
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Best Local Similarity 22.98
Matches 95; Conservative
                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                              NCB1_TaxID=86192;
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Hettwer U., Jaeckel F.R., Boch J., Meyer M., Rudolph K., Ullrich M.S. "Cloning, nucleotide sequence, and expression in Escherichia coli of levansucrase genes from the plant pathogens Pseudomonas syringae pv. glycinea and P. syringae pv. phaseolicola.";
Appl. Environ. Microbiol. 64:3180-3187(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 VWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPTGDNH----IYLLYN----- 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335, YKLNDQRLATATLNLNVDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDRENDDYCL 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 RDPH-VVQLENGDRYLVFEANTGTEDYQSDDQIYNWANYGGDDAFNIKSSFKLLNNKKDR 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVSRGSDRELTAKDNTIVGDNVAMIGYVSDSLMGKYKPLNNSGVVLTASVPANMRTATYS 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 KYGDNDFSHWRN-----AGSIFGTKETNVFQEWSGSAI-VNDDGTIQLFFTSNDTSD
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95;
                                                                                                                                                                                                                                                                                                 Pseudomonas syringae (pv. glycinea).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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J. Bacteriol. 183:3382-3392(2001).
EMBL; AF346402; AAK49952.1;
Transferaes; Glycosyltransferase.
SEQUENCE 431 AA; 47619 MW; 0C71D0F133071AA5 CRC64;
                                                                                                                                                                                                           Last sequence update)
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23.2%; Pred. No. 0.0002;
Live 66; Mismatches 154;
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last sem
LEVANSUCRASE LSCC (EC 2.4.1.10).
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MEDLINE-21242726; PubMed-11344135;
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Best Local Similarity 23.2%
Matches 95; Conservative
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SGLAG 772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 VWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPTGDNHIYL-------LYNKYGD 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDFSHWRN------AGSIFGTKETNVFQEWSGSAI-VNDDGTIQLFFTSNDTSDYKLN 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       459 ANGALGIL---KLTNNQSKPKVEEVYSPLVSTLMACDEVXXK----LGDKYYLFSVTRVS
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                                                                                                                                 Rahnella aquatilis.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 415;
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                                                                                                                                                                                                                                                                             "Cloning and characterization of levansucrase.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AX027657; AX14794-1; -.
Interpro: IRR003469; Glyco_hydro_68.
Pfam: PF02435; Glyco_hydro_68; 1.
SEQUENCE 415 AA; 45958 MW; F09F5A1BF8690C5E CRC64;
                                                                          Last sequence update)
Last annotation update)
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Bacillus/Staphylococcus group; Staphylococcus.
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                                                        Created)
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               PRT;
                                                01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2001 (TrEMBLrel. 18,
          PRELIMINARY;
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Bacteria; Firmicutes; 1
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Best Local Similarity
Matches 92; Conserv
                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Kim H., Cha J.;
                                                                                                                                                                                                NCBI_TaxID=34038;
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in Pathogenicity: a Gene Encoding an Autolysin-Binding Fibronectin and the ica Operon Involved in Biofilm Formation.";

Englic L. Immun. 69:712-718(2001).

EMBL: AR244123; ARX17065.1; -.

InterPro; IPR002502; Amidase_2.

InterPro; IPR002901; Amidase_4.

Pfam: PF01510; Amidase_2: 1.

SMART; SM00047; LYZ2; 1.

SEQUENCE 1395 AA; 153796 MM; IDEC54FA60035F2E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKKTISSLP-KYTPQ-----KASINDYIRKKNY-----KA 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398 NSTIDGEINYMKNNYQ--SAFVHAFVDGNRIVETAPTDY--LSWGAG--PQGNERFINVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      452 IVHTHDY---DSFARSMNNYADY----AATQLQYYGLKPDSAENDGQGTVWTHYAISRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGDDAFNIKSSFKLLNNKKDRELAGLANGALGILKLTNNQSKPKVEEVYSPLVSTLMACD
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Matches 175; Conservative 105; Mismatches 299; Indels 266;
                                                                                                                                                                                                                                                                                                                               Length 1395;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | | : | | : | 258 AKIRFAV-AQPAAVASNNVNDLITVTKQMITEGIKDDGVIQAHDGEHIIYTSDFKIDNAV 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 -----QIGVDGKIISANSNTTSGSTNQESSATNNTENAVVNESKNTNNTENAVVNENKN 104
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Ab Done staloprotein-binding protein from Staphylococcus aureus: a member of the staphylococcus af family ].";
Blochem. J. 345:611-69[2000].
Blochem. J. 18653; CAB75732.1;
InterPro; IPR0011899; Gram_Dos_anchor.
PROSITE; PS00343; GRAM_DOS_ANCHORING; UNKNOWN_1.
SEQUENCE 1171 AA; 127123 MW; C5BC812F9DA5A884 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 KAGDIMIVKYDKETIPSDITDDFTPVDITDPSGEVIAKGTFDLNTKIITYKFTDYVDRYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----NKYGD-NDFSHWRNAGSIFGT--KET--NVFQEWSGSAIVNDDGTIQLFFTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 5.5%; Score 230; DB 2; Length 1171; Best Local Similarity 22.0%; Pred. No. 0.0016; Matches 167; Conservative 103; Mismatches 296; Indels 194;
                                                                                                                                                                (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                        Staphylococcus aureus.

Bacteria: Firmicutes: Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
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MEDLINE-20115096; PubMed-10642520;
                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Create 01-OCT-2000 (TrEMBLrel. 15, Last s 01-JUN-2001 (TrEMBLrel. 17, Last a BONE SIALOPROTEIN-BINDING PROTEIN
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                                                                                                                       PRELIMINARY;
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                                    89 KNTINITENAVVNENKNTINITENAVVNENKNTINITENDINSQLKLTINIEQPSAATQANLKKL 148
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                                                                                                      553 VLTASVP----ANWRTATYSYYAVPVAGHPDQVLIT-----SYMSNKDFASGEGNYAT 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 QKNNMNN--EELSEQNYN----DCNNINKNENNKIDSINNNDNINNNENINNNDSINNN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVQDPVTGYVSNYMGYQLVIAMMGIPNSPTGDNHIYLLYNKYGDNDFSHWRNAGSIFGTK 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INSTREDRINIQFSLDNKIIENNEMKQRNTELLNDNNKIKEIN-KELINEKLYLSKEMEI 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 ESNNYNGVAEVNTERQANGQIGVDGKIISANSNTTSGSTNQESSATNN---TENAVVNES 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>.</u>
149 NPQAAKA-VQNAKIDAGSLTDDQINE------LNKINFSKSAE-----KG
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Plasmodium falciparum (isolate 3D7).
Bukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 73.3 KDA PROTEIN.
                                                                                                                                                                                                          602 WAPSFLVQINPD----DTTTVLARATNQGDWVWDDSSRN 636
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302 TKETNVFQEWSGSAIVNDDGTIQLFFTSNDTSDYKL------
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EMBL; AF362374; AAK54093.1;
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"Identification and cloning of a developmentally regulated
"Identification and cloning of a developmentally regulated
Cryptosportidium parvum gene by differential mRNA display PCR.";
Gene 216:327-334(1998).
EMBL; AR076438; AAC95010.1; -
InterPro; IPR001841; Znf.CCCH.
InterPro; IPR001841; Znf. ing.
Pfam; PF00642; Zf.CCCH; 1.
SMART: SM00184; RING; 1.
SMART: SM001356; Znf. C311; 1.
SEQUENCE 930 Aa; 98563 MW; 5AD78C87FB61F190 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.1%; Score 212.5; DB 5; Length 20.8%; Pred. No. 0.0088; tve 99; Mismatches 307; Indels
                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 17, Last annotation update)
HC-23 PROTEIN.
Cryptosporidium parvum.
Cryptosporidium parvum.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
                                                                                                                                                   930 AA
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MEDLINE-98398455; PubMed-9729442;
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                          518 NNSLLKKKEEQINEYINEI 536
470 NNQSKPKVEEVYSPLVSTL 488
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Matches 174; Conservative
                                                                                                                                                 PRELIMINARY;
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FSVTRV-SRGSDRE-----LTA---KDNTI------VGDNVAMIGYVS--DSLMGKY
                                                                                      545 KPLNNSGVVLTASVPANWRTATYSYYAVPVAGHPDQVLITSYMSNKDFASGEGNYATWAP
                                                                                                                                                                          SFLVQINPDDTTTVLARATNQGDWVWDDSSRNDNMLGVLKEGAANSAALPGEWGKPVDWS
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"The histidine kinases of Dictyostellum.";
(In) Inouye M., Dutta R. (eds.);
HISTIDINE KINASES IN SIGNAL TRASNDUCTION, pp.1-1, Academic press,
                                                                                                                                                                                                                                                                                                                                                            701 PGNGDKPAGKATPDNTNIDPSAQPSGQNTNIDPSAQXSGQNTKNVTPGNEKQGKN 755
                                                                                                                                                                                                                                                                                                                                                                                      Indels 249;
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
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CSTRAIN-ATCC 814, DSM 792 / VKM B-1787;

X MEDLINE-21359325; PubMed-11466286;

A Nobling J. Brefon G., Omelohenko M.V., Makarova K.S., Zeng O.,

A Glbson R., Lee H.M., Dubols J., Qlu D., Hitti J., Wolf Y.I.,

A Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing

"Genome sequence and comparative analysis of the solvent-producing

"Genome sequence and comparative analysis of the solvent-producing

"Bacterium Clostridium acetobutylicum.";

"J Bacteriol. 183:4823-4838(2001).

R FMBL; AEO07623; AAK79053:1;

R InterPro; IPR002479; CW_binding.

R Fmm; PF01473; CW_binding...

R Complete proteome.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 KDRELAGLANGALGILKLTNNQSKPKVEEVYSPLVSTLMACDEVXXKLGDKYYLFSVTRV 510
| ||| : : : | | | | 494 FK---VFQRTTFQSAI-----YFFNERNGDFNLILLDPLIPSLVIDEIKQMKQDSSN 542
                                                                                                                        -----LATAIL--NLNVDDNGVSIKSVDNYQVLFEGDGFHYQTYEQFANGKDREND 390
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         736 QXSGQ------NTK--NVTPGNEKQGKNTDAK------QLPQTGNKS 768
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNCHARACTERIZED PROTEIN, RELATED TO ENTEROTOXINS OF
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34 NNYNGVAEVNT-----ERQA--NGQIGVDGKIISANSNTTSGSTNQESSA--TNNT 80

Matches 143; Conservative

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STRAIN=NEWMAN;
MEDLINE-99098700; PubMed-9884231;
Josefsson E., McCrea K., Ni Eidhin D., O'Connell D., Cox J., Hook M.,
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66 NNLNTKVQTNTASSSMPNTNPKQATNNSKILVNPKLNQASSPNEGITPKKQASIPYTNVT 125
                                                                           D---NSQLKLT------NNEQPSAATQANLKKLNPQAAKAVQNAKIDAGSLTDD 169
                                                                                                                                                                                                                      --QT-----YEQFANGKDRENDDYCLRDPHVVQLENGDRYLVFEAN------ 414
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                                                   ENAVVNESKNTNNTENAVVNE----NKNTNNT------ENAVVNENKNTNNTEN 124
                                                                                                                                                                                               170 QINELNKINFSKSAEKGAKLTFKDLEGIGNAIVKQDPQYAIPYSNAKEIK-----NMPAT 224
                                                                                                                                                                                                                                                                     YTVD---AQTGKMAHLDVWDSWPVQDPVTGYVSNYMGYQLVIAMMGIPNSPTGDNHIYLL 281
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Microbiology 144:3387-3395(1998).
EmbL, AJ005647; CAA06652.1; -.
InterPro; IPR001899; Gram_pos_anchor.
                                                                                                                                                                                                                                                                                                         YFNDDGSMQTG------TGLQNINGT
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                                                                                                                                                                                                                                                                                                                                                                                                                 341 RLATATLNLNVDDNG-----VSIKSVDNYQVLFEG------DGFHY----
                                                                                                                                              532 MIGYVSDSLMGKYKPLNNSGVVLTASVPANWRTATYSYYAVPVAGHPDQVLITSYMSNK
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PROSITE; PS00343; GRAM POS ANCHORING; UNKNOWN 1.
SEQUENCE 1166 AA; 126548 MW; 750A7B0135287D4A CRC64;
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Bacteria; Firmicutes; Bacillus/Clostridium gro
Bacillus/Staphylococcus group; Staphylococcus.
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